=> file medline FILE 'MEDLINE' ENTERED AT 12:07:23 ON 28 JUL 2003

FILE LAST UPDATED: 26 JUL 2003 (20030726/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/changes2003.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

terminology

Nt = narrower term

B1 = Biosynthesis

IP = isolation &

OR purification

=> d que 149

PLU=ON CAROTENOIDS+NT/CT L43 37021 SEA FILE=MEDLINE ABB=ON 82158 SEA FILE=MEDLINE ABB=ON PLU=ON OXYGEN/CT

2 cites

L44 1414 SEA FILE=MEDLINE ABB=ON PLU=ON L43(L)(BI OR IP)/CT L47

41 SEA FILE=MEDLINE ABB=ON L48 149

PLU=ON L47 AND L44 2 SEA FILE=MEDLINE ABB=ON PLU=ON L48 AND (BIOGENESIS OR

=> file caba

FILE 'CABA' ENTERED AT 12:07:25 ON 28 JUL 2003 COPYRIGHT (C) 2003 CAB INTERNATIONAL (CABI)

GIGANTEUS)/TI

FILE COVERS 1973 TO 7 Jul 2003 (20030707/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d aue 167

L63	15147	SEA FILE=CABA ABB=ON PLU=ON CAROTEN?
L64	884	SEA FILE=CABA ABB=ON PLU=ON L63 AND (CULTUR? OR FERMENT?)
L65	8723	SEA FILE=CABA ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR
		AERAT?)(5A)(VARY? OR CONTROL? OR LEVEL OR UPTAK? OR CONENTRAT?
		OR AMOUNT)
L66	7	SEA FILE=CABA ABB=ON PLU=ON L64 AND L65
L67	1	SEA FILE=CABA ABB=ON PLU=ON L66 AND SUCCINATE/TI 1 Citc

=> file biotechno

FILE 'BIOTECHNO' ENTERED AT 12:07:26 ON 28 JUL 2003 COPYRIGHT (C) 2003 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE LAST UPDATED: 22 JUL 2003 <20030722/UP> FILE COVERS 1980 TO DATE.

SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN /CT AND BASIC INDEX <<<

=> d que 158

L53	2639 SEA	FILE=BIOTECHNO ABB=ON	i PLU=ON	?CAROTEN?
L54	393 SEA	FILE=BIOTECHNO ABB=ON	N PLU=ON	L53 AND (CULTUR? OR

	FERMENT?)
L55	73 SEA FILE=BIOTECHNO ABB=ON PLU=ON L54 AND (OXYGEN? OR AEROB?
	OR O2 OR AERAT?)
L56	4620 SEA FILE=BIOTECHNO ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR
	AERAT?)(5A)(VARY? OR CONTROL? OR CONCENTRAT? OR AMOUNT)
L57	10 SEA FILE=BIOTECHNO ABB=ON PLU=ON L55 AND L56
L58	3 SEA FILE=BIOTECHNO ABB=ON PLU=ON LS7 AND (FOAM OR STOICHIOMET 3 cites
	RIC OR GLUT?)/TI

=> file hcaplus

L12

L13

L14

L15

L16

L17

L18

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FILE COVERS 1907 - 28 Jul 2003 VOL 139 ISS 5 FILE LAST UPDATED: 27 Jul 2003 (20030727/ED)

7229 SEA FILE=HCAPLUS ABB=ON

78324 SEA FILE=HCAPLUS ABB=ON

317219 SEA FILE=HCAPLUS ABB=ON

8976 SEA FILE=HCAPLUS ABB=ON

373 SEA FILE=HCAPLUS ABB=ON

7 SEA FILE=HCAPLUS ABB=ON

This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> d que 118
                                                                                                   all of the cpds indexed in the cite for applicantly provity document
                        42 SEA FILE=REGISTRY ABB=ON PLU=ON (472-61-7/BI OR 4418-73-9/BI
         L5
                           OR 144-68-3/BI OR 432-68-8/BI OR 4339-77-9/BI OR 4418-72-8/BI
                           OR 514-78-3/BI OR 7235-40-7/BI OR 472-70-8/BI OR 108-20-3/BI
                           OR 108-88-3/BI OR 108-94-1/BI OR 109-99-9/BI OR 110-54-3/BI OR
                           110-82-7/BI OR 110-86-1/BI OR 116-30-3/BI OR 123-86-4/BI OR
                            123-91-1/BI OR 1330-20-7/BI OR 141-78-6/BI OR 142-82-5/BI OR
all constenseds
in expels cited
                            162875-45-8/BI OR 19866-02-5/BI OR 222713-29-3/BI OR 334071-56-
                           6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR
                           472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR
                           64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR
                           71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR
                           78-93-3/BI)
                        18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES want cpds w [] 15 SEA FILE=REGISTRY ARR-ON PLU=ON L8 NOT 46 150 18/PTD.
                                                        PLU=ON L8 NOT 46.150.18/RID - no
                        15 SEA FILE=REGISTRY ABB=ON
                                                                                                    (a) rings
                                                       PLU=ON 7782-44-7 - 02
PLU=ON CAROTENES+PFT,NT/CT
         L10
                         1 SEA FILE=REGISTRY ABB=ON
         L11
                     32232 SEA FILE=HCAPLUS ABB=ON
                                                                                              PFT = old, now &
"used for" terms
preparative role
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                                                       PLU=ON L9
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L10

PLU=ON

PLU=ON

PLU=ON

PLU=0N

(L11 OR L12)(L)PREP/RL

CULTURE MEDIA +PFT/CT

L13 AND (L14 OR L15)

PLU=ON FERMENTATION+PFT/CT

PLU=ON L16 AND L17 7 cites

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=> d que 122
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                6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR
                472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR
                64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR
                71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR
                78-93-3/BI)
L8
             18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES
L9
             15 SEA FILE=REGISTRY ABB=ON
                                         PLU=ON L8 NOT 46.150.18/RID
          32232 SEA FILE=HCAPLUS ABB=ON
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L11
          66957 SEA FILE=HCAPLUS ABB=ON
                                                 L9
L12
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L13
           7229 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
                                                 (L11 OR L12)(L)PREP/RL
          78324 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
                                                 FERMENTATION+PFT/CT
L14
L15
           8976 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
                                                 CULTURE MEDIA +PFT/CT
            373 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
L16
                                                 L13 AND (L14 OR L15)
L19
           2187 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
                                                 BUBBLING/CT
L20
           1915 SEA FILE=HCAPLUS ABB=ON
                                         PLU=ON
                                                 AERATION/CT
L21
            365 SEA FILE=HCAPLUS ABB=ON PLU=ON AERATORS/CT
                                         PLU=ON L16 AND (L19 OR L20 OR L21) 3 cites
              3 SEA FILE=HCAPLUS ABB=ON
L22
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=> s 118 or 122

L79 8 L18 OR L22 8 cites total for HCAPLUS

=> file wpix

FILE 'WPIX' ENTERED AT 12:07:30 ON 28 JUL 2003 COPYRIGHT (C) 2003 THOMSON DERWENT

FILE LAST UPDATED: 23 JUL 2003 <20030723/UP>
MOST RECENT DERWENT UPDATE: 200347 <200347/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

- >>> NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <<<
- >>> SLART (Simultaneous Left and Right Truncation) is now
 available in the /ABEX field. An additional search field
 /BIX is also provided which comprises both /BI and /ABEX <<<</pre>
- >>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<
- >>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES,
 SEE http://www.derwent.com/dwpi/updates/dwpicov/index.html <<<</pre>
- >>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
 PLEASE VISIT:
 http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<</pre>
- >>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
 GUIDES, PLEASE VISIT:

http://www.derwent.com/userguides/dwpi_guide.html <<<

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=> d que 133
L24
          3123 SEA FILE=WPIX ABB=ON PLU=ON ?CAROTEN?
L25
         40704 SEA FILE=WPIX ABB=ON
                                    PLU=ON ?FERMENT?
L26
          1546 SEA FILE=WPIX ABB=ON
                                     PLU=ON CULTUR? MEDIA
L27
         37669 SEA FILE=WPIX ABB=ON
                                     PLU=ON MICROB?
L28
           236 SEA FILE=WPIX ABB=ON
                                     PLU=ON L24 AND (L25 OR L26 OR L27)
L29
            15 SEA FILE=WPIX ABB=ON
                                     PLU=ON L28 AND OXYGEN
L30
             1 SEA FILE=WPIX ABB=ON
                                     PLU=ON L28 AND O2
L31
            16 SEA FILE=WPIX ABB=ON
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L32
            11 SEA FILE=WPIX ABB=ON
                                     PLU=ON L31 NOT (SKIN OR DOUGH OR
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L33
             4 SEA FILE=WPIX ABB=ON PLU=ON L32 AND ( CANTHAXANTHIN OR
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=> d que 140
L24
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L25
         40704 SEA FILE=WPIX ABB=ON PLU=ON ?FERMENT?
L26
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                                    PLU=ON CULTUR? MEDIA
                                    PLU=ON MICROB?
L27
         37669 SEA FILE=WPIX ABB=ON
L28
           236 SEA FILE=WPIX ABB=ON
                                     PLU=ON L24 AND (L25 OR L26 OR L27)
L29
            15 SEA FILE=WPIX ABB=ON
                                    PLU=ON L28 AND OXYGEN
                                     PLU=ON L28 AND O2
L30
             1 SEA FILE=WPIX ABB=ON
                                     PLU=ON (L29 OR L30)
L31
            16 SEA FILE=WPIX ABB=ON
L36
           685 SEA FILE=WPIX ABB=ON
                                    PLU=ON L24(5A) (PRODUC? OR PREP?)
            46 SEA FILE=WPIX ABB=ON
                                     PLU=ON L36 AND OXYGEN?
L37
            19 SEA FILE=WPIX ABB=ON
                                    PLU=ON L37 AND (MICROB? OR L25 OR
L38
               CULTUR?)
L39
            11 SEA FILE=WPIX ABB=ON PLU=ON L38 NOT L31
             1 SEA FILE-WPIX ABB-ON PLU-ON L39 AND STIRRING/TI / c;+e
L40
=> s 133 or 140
            5 L33 OR L40 5 cites total for WPIX
=> dup rem 149 167 158 179 180 removing duplicate citations
FILE 'MEDLINE' ENTERED AT 12:08:32 ON 28 JUL 2003
FILE 'CABA' ENTERED AT 12:08:32 ON 28 JUL 2003
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FILE 'BIOTECHNO' ENTERED AT 12:08:32 ON 28 JUL 2003
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PROCESSING COMPLETED FOR L49
PROCESSING COMPLETED FOR L67
PROCESSING COMPLETED FOR L58
PROCESSING COMPLETED FOR L79
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PROCESSING COMPLETED FOR L80
             17 DUP REM L49 L67 L58 L79 L80 (2 DUPLICATES REMOVED) 17 cites total
L81
                ANSWERS '1-2' FROM FILE MEDLINE
                ANSWER '3' FROM FILE CABA
                ANSWERS '4-6' FROM FILE BIOTECHNO
                ANSWERS '7-12' FROM FILE HCAPLUS
                ANSWERS '13-17' FROM FILE WPIX
=> d ibib abs ind 1-2
                         -indexing
L81 ANSWER 1 OF 17
                        MEDLINE on STN
ACCESSION NUMBER:
                    74298770
                                 MEDLINE
DOCUMENT NUMBER:
                    74298770
                               PubMed ID: 4850775
TITLE:
                    Biogenesis of beta-carotene in Mycobacterium
                    kansasii.
AUTHOR:
                    David H L
SOURCE:
                    JOURNAL OF BACTERIOLOGY, (1974 Aug) 119 (2) 527-33.
                    Journal code: 2985120R. ISSN: 0021-9193.
                    Report No.: NASA-74298770.
PUB. COUNTRY:
                    United States
DOCUMENT TYPE:
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:
FILE SEGMENT:
                    Priority Journals; Space Life Sciences
ENTRY MONTH:
                    197410
ENTRY DATE:
                    Entered STN: 19900310
                    Last Updated on STN: 19900310
                    Entered Medline: 19741025
                                                                 no abstract given
CT
      Acetates: ME, metabolism
      Amines: PD, pharmacology
      Biogenesis
      Carbon Radioisotopes
       *Carotenoids: BI, biosynthesis
      Chloramphenicol: PD, pharmacology
      Chromatography, Thin Layer
      Darkness
      Light
     *Mycobacterium: ME, metabolism
        0xygen
      RNA, Bacterial: BI, biosynthesis
      Rifampin: PD, pharmacology
      Spectrophotometry
      Temperature
      Time Factors
      Tritium
      Uracil: ME, metabolism
     10028-17-8 (Tritium); 13292-46-1 (Rifampin); 36-88-4 (Carotenoids);
RN
     56-75-7 (Chloramphenicol); 66-22-8 (Uracil); 7782-44-7 (Oxygen)
     O (Acetates); O (Amines); O (Carbon Radioisotopes); O (RNA, Bacterial)
CN
L81 ANSWER 2 OF 17
                        MEDLINE on STN
ACCESSION NUMBER:
                                 MEDLINE
                    73227417
DOCUMENT NUMBER:
                    73227417
                               PubMed ID: 4665108
                    Studies on natural photo-protectors. II. The influence of
TITLE:
                    oxygen and temperature on photosensitivity of mutants of
                    Aspergillus giganteus with various ability of
                    carotenoid synthesis.
AUTHOR:
                    Lazarski R
                    FOLIA BIOLOGICA, (1972) 20 (3) 279-86.
SOURCE:
                    Journal code: 2984758R. ISSN: 0015-5497.
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PUB. COUNTRY:

Poland Poland

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

197310

ENTRY DATE:

Entered STN: 19900310

Last Updated on STN: 19900310

Entered Medline: 19731005

CT Aerobiosis
Anaerobiosis

*Aspergillus: ME, metabolism *Carotenoids: BI, biosynthesis

Genetics, Microbial

*Light Mutation *Oxygen

*Temperature

RN 36-88-4 (Carotenoids); 7782-44-7 (Oxygen)

=> d ibib abs ind 3

L81 ANSWER 3 OF 17 CABA COPYRIGHT 2003 CABI on STN

ACCESSION NUMBER:

83:112346 CABA

DOCUMENT NUMBER:

831980736

TITLE:

The role of oxygen concentration in the synthesis of

carotenoids, poly- beta -hydroxybutyrate and

succinate oxidase in continuous

culture of Azospirillum

AUTHOR:

SOURCE:

Nur, I.; Okon, Y.; Henis, Y. Dep. of Plant Path. and Microbiology, Hebrew Univ.

CORPORATE SOURCE:

of Jerusalem, P.O. Box 12, Rehovot 76100, Israel. Israel Journal of Botany, (1982) Vol. 31, No. 1-4,

pp. 221-227. 19 ref.

ISSN: 0021-213X

DOCUMENT TYPE:

Conference Article; Journal

LANGUAGE:

English

AB Azospirillum brasilense strain Cd was grown in ammonium-malate-mineral salts medium under various dissolved oxygen tensions. Maximum poly- beta -hydroxybutyrate content was observed under microaerobic conditions and intermediate dilution rates. Highest cell yield and respiration rate were obtained at relatively low oxygen. Protein content was higher at high oxygen levels. Succinate oxidase and succinate dehydrogenase activities were especially high under high oxygen. Four carotenoids were isolated and purified from membranes. In the

presence of diphenylamine which inhibits carotenoid synthesis, the rate of acetylene reduction decreased to 50% of the control. In liquid

cultures, carotenoid synthesis was initiated only after the depletion of NH4Cl when N2 fixing activity became evident.

Carotenoids appeared to protect nitrogenase from oxidative damage. EE110 Agricultural Economics; DD500 Laws and Regulations; DD100 Administration of Agencies and Organizations; CC200 Extension and Advisory

Work; UU000 Sociology (General); JJ100 Soil Biology

BT prokaryotes; Azospirillum; Spirillaceae; Gracilicutes; bacteria

CT Nitrogen Fixation; enzymes; oxygen

ST specific taxa

RN 7782-44-7

CC

ORGN bacteria; Azospirillum brasilense

=> d ibib abs ind 4-6

ANSWER 4 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN L81 DUPLICATE ACCESSION NUMBER: 1999:30021700 **BIOTECHNO** Control of both foam and dissolved TITLE: oxygen in the presence of a surfactant for production of .beta.-carotene in Blakeslea trispora AUTHOR: Seon-Won K.; Lee I.-Y.; Jeong J.-C.; Lee J.-H.; Park Y.-H. CORPORATE SOURCE: I.-Y. Lee, Bioprocess Technol. Res. Division, Korea Res. Inst. of Biosci./Biotech., P.O. Box 115, Yusong, Taejon 305-600, South Korea. E-mail: leeiy@mail.kribb.re.kr SOURCE: Journal of Microbiology and Biotechnology, (1999), 9/5 (548-553), 20 reference(s) CODEN: JOMBES ISSN: 1017-7825 DOCUMENT TYPE: Journal: Article COUNTRY: Korea, Republic of English LANGUAGE: SUMMARY LANGUAGE: English 1999:30021700 **BIOTECHNO** ΑN A production of .beta.-carotene was attempted in a fed-batch AΒ culture of Blakeslea trispora by controlling both foam and dissolved oxygen in the presence of surfactant, Span 20. Results obtained from the shake flask cultures indicated that a high concentration of dissolved oxygen was needed for both cell growth and .beta.-carotene synthesis, and the optimal concentration of glucose was found to be in the range of 50-100 g/l. In order to maintain the dissolved oxygen concentration level at higher than 50% of air saturation, pure oxygen was automatically sparged into the medium with air. Foam was controlled by bypassing air from the submerged aeration to the headspace in response to the foam that was caused by Span 20. High agitation speed was found to be detrimental to the cell growth due to shear damage, even though it provided sufficient dissolved oxygen. On the other hand, a low aeration speed caused stagnant regions in the fermentor because of improper mixing. Thus, for the fed-batch operation, agitation speed was increased gradually from 300 to 700 rpm to prevent cell damage at the initial stage of fermentation and to give efficient mixing for a viscous culture broth as the culture proceeded. By controlling dissolved oxygen and foam, a high concentration of .beta.carotene (1,190 mg/l) was obtained in 6 days of the fed-batch culture of B. trispora with 2.5% of the dry cell weight, which was approximately 5 times higher than that of the batch cultures CT*dissolved oxygen; *surfactant; *sorbitan laurate; *beta carotene; *biotechnology; *protein synthesis; * fermentation; *fungus; *blakeslea trispora; glucose; foam; oxygen concentration; shear stress; bioreactor; fungus mutant; light exposure; oxidative stress; centrifugation; high performance liquid chromatography; mycelium; cell growth; nonhuman; article (sorbitan laurate) 1338-39-2; (beta carotene) 7235-40-7; RN (glucose) 50-99-7, 84778-64-3 ANSWER 5 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN L81 DUPLICATE ACCESSION NUMBER: 1997:27485777 **BIOTECHNO**

TITLE: Influence of oxygen and glucose on primary

metabolism and astaxanthin production by Phaffia

rhodozyma in batch and fed-batch cultures:

Kinetic and stoichiometric analysis

AUTHOR: Yamane Y.-I.; Higashida K.; Nakashimada Y.; Kakizono

T.; Nishio N.

CORPORATE SOURCE:

N. Nishio, Fermentation Technology Department, Faculty

of Engineering, Hiroshima University, Kagamiyama

1-4-1, Higashi-Hiroshima 739, Japan. E-mail: nnishio@ipc.hiroshima-u.ac.jp

SOURCE:

Applied and Environmental Microbiology, (1997), 63/11

(4471-4478), 35 reference(s) CODEN: AEMIDF ISSN: 0099-2240

DOCUMENT TYPE:

Journal; Article

COUNTRY:

United States

LANGUAGE:

English

SUMMARY LANGUAGE:

English

AN 1997:27485777

BIOTECHNO

AB The influence of the oxygen and glucose supply on primary metabolism (fermentation, respiration, and anabolism) and

astaxanthin production in the yeast Phaffia rhodozyma was investigated.

When P. rhodozyma grew under fermentative conditions with limited oxygen or high concentrations of glucose, the

astaxanthin production rate decreased remarkably. On the other hand, when

the yeast grew under **aerobic** conditions, the astaxanthin production rate increased with increasing **oxygen** uptake. A

kinetic analysis showed that the respiration rate correlated positively with the astaxanthin production rate, whereas there was a negative correlation with the ethanol production rate. The influence of glucose

concentration at a fixed nitrogen concentration with a high level of oxygen was then investigated. The results showed that

astaxanthin production was enhanced by an initial high carbon/nitrogen ratio (C/N ratio) present in the medium, but cell growth was inhibited by a high glucose concentration. A stoichiometric analysis suggested that astaxanthin production was enhanced by decreasing the amount of NADPH required for anabolism, which could be achieved by the repression of protein biosynthesis with a high C/N ratio. Based on these results, we performed a two-stage fed-batch culture, in which cell growth was enhanced by a low C/N ratio in the first stage and astaxanthin

production was enhanced by a high C/N ratio in the second stage. In this culture system, the highest astaxanthin production, 16.0 mg per

liter, was obtained.

RN (astaxanthin) 472-61-7; (carbon) 7440-44-0; (glucose) 50-99-7, 84778-64-3; (nitrogen) 7727-37-9; (oxygen) 7782-44-7; (reduced

nicotinamide adenine dinucleotide phosphate) 53-57-6

L81 ANSWER 6 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN

ACCESSION NUMBER:

1999:29160364 BIOTECHNO

TITLE:

Effect of culture condition on the

biosynthesis of carotenoids in Rhodotorula

glutinis No. 21

AUTHOR:

Sakaki H.; Nochide H.; Nakanishi T.; Miki W.; Fujita

T.; Komemushi S.

CORPORATE SOURCE:

H. Sakaki, Department of Agricultural Chemistry, Faculty of Agriculture, Kinki University, 3327-204

Nakamachi, Nara 631-8505, Japan.

SOURCE:

Seibutsu-kogaku Kaishi, (1999), 77/2 (55-59), 13

reference(s)

CODEN: SEKAEA ISSN: 0919-3758

DOCUMENT TYPE:

Journal: Article

COUNTRY:

Japan

LANGUAGE:

Japanese

SUMMARY LANGUAGE:

English; Japanese

AN 1999:29160364 BIOTECHNO

AB Changes in the biosynthesis of carotenoids caused by altering the culture conditions of the yeast Rhodotorula glutinis No. 21 were investigated. Cells grown on lactate showed a higher production of torularhodin, one of the final products, compared with those grown on glucose, but no changes were observed as a result of adjusting the pH, at the start of the cultivation. These findings suggested that the difference in the carbon source was a factor giving rise to a change in the carotenoid biosynthesis system of R. glutinis No. 21. Increases in the contents of torulene and torularhodin were related to elevation of the dissolved oxygen concentration, which was adjusted by aeration. It was concluded that this yeast switches its system of carotenoid biosynthesis according to the extracellular conditions. The results obtained will contribute to elucidating the role of torularhodin in this non-phototrophic yeast which produces two carotenoids, .beta.-carotene and torularhodin, as the final products.

CT*biosynthesis; *carotenoid; *Rhodotorula glutinis; lactic acid; torularhodin; glucose; pH; torulene; dissolved oxygen;

aeration; beta carotene

=> d ibib abs hitrn ind 7-12

L81 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2003:320046 HCAPLUS

DOCUMENT NUMBER:

138:302755

TITLE:

Microorganism and production of carotenoid compounds

thereby

INVENTOR(S):

Yamaoka, Yukiho

PATENT ASSIGNEE(S):

National Institute of Advanced Industrial Science and

Technology, Japan

SOURCE:

PCT Int. Appl., 24 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

Japanese

FAMILY ACC. NUM. COUNT:

JP 2003189846

PRIORITY APPLN. INFO.:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003033683 W: CN, US	A1	20030424	WO 2002-JP10619	20021011

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR

A2 20030708 JP 2002-231126 20020808 JP 2001-318746 A 20011016 JP 2002-132190

A 20020507 A 20020808 JP 2002-231126

Astaxanthin and canthaxanthin are manufd. com. with marine ΑB Thraustochytrium sp. CHN-3 (FERM P-18556) of Labyrinthula by aerobic fermn. under illumination. The astaxanthin and canthaxanthin are isolated from the microorganism by solvent extn. and chromatog.

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IT
    7782-44-7, Oxygen, biological studies
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
IC
    ICM C12N001-14
     ICS C12P023-00; C12R001-645
CC
     16-2 (Fermentation and Bioindustrial Chemistry)
     Section cross-reference(s): 1, 17, 63
     astaxanthin canthaxanthin manuf Thraustochytrium Labyrinthula culture
ST
    medium
     Fermentation
IT
        (aerobic; astaxanthin andcanthaxanthin manuf. with marine
        Thraustochytrium)
IT
     Carbon sources, microbial
      Culture media
    Feed
     Health food
     Illumination
     Labyrinthula
     Nitrogen sources, microbial
     Seawater
     Solvent extraction
     Thraustochytrium
        (astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
IT
    Carotenes, preparation
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
IT
     Vitamins
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
IT
    Light
        (blue; astaxanthin andcanthaxanthin manuf. with marine
        Thraustochytrium)
IT
    Light
        (red; astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
     50-99-7, D-Glucose, biological studies 57-13-6, Urea, biological studies
TT
     57-48-7, D-Fructose, biological studies 57-50-1, Sucrose, biological
              59-43-8, Thiamine, biological studies 67-56-1, Methyl alcohol,
     biological studies 67-64-1, Acetone, biological studies
                                                                 67-66-3.
                                     7664-41-7, Ammonia, biological studies
     Chloroform, biological studies
     7757-79-1, Potassium nitrate, biological studies 7782-44-7,
     Oxygen, biological studies
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (astaxanthin andcanthaxanthin manuf. with marine Thraustochytrium)
REFERENCE COUNT:
                               THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L81 ANSWER 8 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
                         2002:181867 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         138:236950
                         Effect of the aeration rate and agitation speed on
TITLE:
                         .beta.-carotene production and morphology of Blakeslea
                         trispora in a stirred tank reactor: mathematical
                         modeling
                         Mantzouridou, F.; Roukas, T.; Kotzekidou, P.
AUTHOR(S):
CORPORATE SOURCE:
                         Department of Food Science and Technology, Aristotle
```

University of Thessaloniki, Thessaloniki, 54006,

Greece

SOURCE: Biochemical Engineering Journal (2002), 10(2), 123-135

CODEN: BEJOFV; ISSN: 1369-703X

PUBLISHER:

Elsevier Science S.A.

DOCUMENT TYPE:

Journal

LANGUAGE: Enalish

The effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in a stirred tank reactor was investigated. B. trispora formed hyphae, zygophores and zygospores during the fermn. The zygospores were the morphol. form responsible for .beta.-carotene prodn. Both aeration and agitation significantly affected .beta.-carotene concn., productivity, biomass and the volumetric mass transfer coeff. (KLa). The highest .beta.-carotene concn. (1.5 kg m-3) and the highest productivity (0.08 kg m-3 per day) were obtained at low impeller speed (150 rpm) and high aeration rate (1.5 vvm). Also, max. productivity (0.08 kg m-3 per day) and biomass dry wt. (26.4 kg m-3) were achieved at high agitation speed (500 rpm) and moderate aeration rate (1.0 vvm). Conversely, the highest value of KLa (0.33 s-1) was obsd. at high agitation speed (500 rpm) and high aeration rate (1.5 vvm). The expts. were arranged according to a central composite statistical design. Response surface methodol. was used to describe the effect of impeller speed and aeration rate on the most important fermn. parameters. In all cases, the fit of the model was found to be good. All fermn. parameters (except biomass concn.) were strongly affected by the interactions among the operation variables. .beta.-Carotene concn. and productivity were significantly influenced by the aeration, agitation, and by the pos. or neg. quadratic effect of the aeration rate. Biomass concn. was principally related to the aeration rate, agitation speed, and the pos. or neg. quadratic effect of the impeller speed and aeration rate, resp. Finally, the volumetric mass transfer coeff. was characterized by the significant effect of the agitation speed, while the aeration rate had a small effect on KLa.

IT 7782-44-7, Oxygen, processes

RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process) (dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

TT **7235-40-7P**, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

CC16-2 (Fermentation and Bioindustrial Chemistry)

ST Blakeslea beta carotene fermn aeration agitation model

IT

(batch; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Mass transfer

> (gas-liq., KLa; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Aeration

Agitation (mechanical) Blakeslea trispora Cell morphology

Simulation and Modeling, biological

(modeling of the effect of aeration rate and agitation speed on

.beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Optimization

(statistical; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Fermentation apparatus

(stirred-tank fermentor; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT 7782-44-7, Oxygen, processes

RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process) (dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT **7235-40-7P**, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

REFERENCE COUNT:

17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 9 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2001:924027 HCAPLUS

DOCUMENT NUMBER:

136:52783

TITLE:

Process for producing carotenoid pigments

INVENTOR(S): Tsubok

Tsubokura, Akira; Mizuta, Haruyoshi Nippon Mitsubishi Oil Corporation, Japan

PATENT ASSIGNEE(S): SOURCE:

PCT Int. Appl., 23 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent Japanese

LANGUAGE: FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

	PATENT NO.	KIND DAT	E	APPLICATION NO.	DATE
					20040600
	WO 2001096591			WO 2001-JP4874	20010608
	W: AU, CA,		•		
	RW: AT, BE,	CH, CY, DE	, DK, ES, F	I, FR, GB, GR, II	E, IT, LU, MC, NL,
	PT, SE,	TR			
	JP 2001352995	A2 200	11225	JP 2000-175124	20000612
	AU 2001062730	A5 200	11224	AU 2001-62730	20010608
	EP 1229126	A1 200	20807	EP 2001-936932	20010608
	R: AT, BE,	CH, DE, DK	, ES, FR, C	B, GR, IT, LI, L	J, NL, SE, MC, PT,
	IE, FI,	CY, TR			
	US 2003044886	A1 200	30306	US 2002-49228	20020211
PRIOR	RITY APPLN. INFO	.:	JP	2000-175124 A	20000612
			WC	2001-JP4874 W	20010608
AR	A process for t	he microbia	1 manuf. of	carotenoids of	desired ratio of

- AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given. The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a liq. culture medium during the fermn.
- IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone 472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

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514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
     4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
     7235-40-7P, .beta.-Carotene
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (process for producing carotenoid pigments)
IT
     7782-44-7, Oxygen, biological studies
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (process for producing carotenoid pigments)
IC
     ICM C12P023-00
     16-2 (Fermentation and Bioindustrial Chemistry)
CC
ST
     carotenoid manuf bacteria dissolved oxygen
IT
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (16 S, gene for; process for producing carotenoid pigments)
     Bacteria (Eubacteria)
IT
       Culture media
     DNA sequences
       Fermentation
     Taxonomy
        (process for producing carotenoid pigments)
IT
     Carotenes, preparation
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (process for producing carotenoid pigments)
     Gene, microbial
TT
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (process for producing carotenoid pigments)
IT
     382660-64-2
                   382660-65-3
     RL: PRP (Properties)
        (nucleotide sequence; process for producing carotenoid pigments)
     144-68-3P, Zeaxanthin 432-68-8P, Echinenone
TT
     472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
     514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
     4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
     7235-40-7P, .beta.-Carotene
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (process for producing carotenoid pigments)
     7782-44-7, Oxygen, biological studies
IT
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (process for producing carotenoid pigments)
REFERENCE COUNT:
                         12
                               THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L81 ANSWER 10 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                         2001:691371 HCAPLUS
                         135:370671
DOCUMENT NUMBER:
TITLE:
                         Application of a complete factorial design for the
                         production of zeaxanthin by Flavobacterium sp.
                         Masetto, Alejandra; Flores-Cotera, Luis B.; Diaz,
AUTHOR(S):
                         Carlos; Langley, Elizabeth; Sanchez, Sergio
CORPORATE SOURCE:
                         Departamento de Biologia Molecular y Biotecnologia del
                         Instituto de Investigaciones Biomedicas, Universidad
                         Nacional Autonoma de Mexico, Mexico, 04510, Mex.
                         Journal of Bioscience and Bioengineering (2001),
SOURCE:
                         92(1), 55-58
                         CODEN: JBBIF6; ISSN: 1389-1723
PUBLISHER:
                         Society for Bioscience and Bioengineering, Japan
```

DOCUMENT TYPE:

Journal English

LANGUAGE: English

AB Utilizing a four-liter fermentor and applying a complete factorial design 23, the combined effects of agitation speed, aeration rate, and corn steep liquor concn. on zeaxanthin prodn. by Flavobacterium sp. were studied.

Maximum growth and prodn. of total carotenoids and zeaxanthin were obtained at 600 rpm, 2 vvm and 4.6% corn steep liquor. Under these conditions, zeaxanthin represented 86% of the total carotenoids produced. Lower values of the variables studied resulted in lower growth, volumetric prodn. of zeaxanthin and total carotenoids, and favored the formation of other carotenoids such as .beta.-carotene and canthaxanthin. The pos. effects on growth and total carotenoids and zeaxanthin formation were in a large extent due to the interaction of agitation/corn steep liquor. However, aeration also had a pos. effect on growth.

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST Flavobacterium zeaxanthin fermn optimization

IT Fermentation

(aerobic; application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT Aeration

Agitation (mechanical)

Flavobacterium

Growth, microbial

(application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT Carotenes, preparation

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT Industrial liquors

(corn steep liquor; application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT Optimization

(statistical; application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by Flavobacterium sp.)

REFERENCE COUNT:

THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN ACCESSION NUMBER: 2002:118119 HCAPLUS DOCUMENT NUMBER: 136:133689 TITLE: Production of .beta.-carotene from Blakeslea trispora Park, Yeong Hoon; Lee, In Yeong; Kim, Seon Won; Lee, INVENTOR(S): Jung Heon; Jeong, Jae Cheol PATENT ASSIGNEE(S): Korea Institute of Science and Technology, S. Korea SOURCE: Repub. Korean Kongkae Taeho Kongbo, No pp. given CODEN: KRXXA7 DOCUMENT TYPE: Patent LANGUAGE: Korean FAMILY ACC. NUM. COUNT: PATENT INFORMATION: PATENT NO. KIND DATE APPLICATION NO. DATE KR 2000031738 Α 20000605 KR 1998-47930 19981110 PRIORITY APPLN. INFO.: KR 1998-47930 Addn. of a surfactant in the medium to increase the prodn. of .beta.-carotene by a Blakeslea trispora culture causes foaming during fermn. An anti-foaming agent can be used to control foam, but it inhibits the growth of the fungi. Submerged aeration accompanied with surface aeration and control of stirring speed can be used effectively to control foam and increase the yield of .beta.-carotene from Blakeslea. In the fermn. process, the anti-foam agent, Span 20 is used to control foam. In addn. to anti-foam agent, submerged and surface aeration are applied to control foam. The total aeration rate is controlled in the range of 0.5-3.0 L air/L medium/min depending on the growth state of fungi. The speed of stirring is increased stepwise in the range of 10-100 rpm reached at 150-800 rpm depending on the increase of cell mass. The main source of carbon is glucose and the optimal concn. is kept under 70 g/L supplied intermittently. Pure oxygen is supplied to increase the dissolved oxygen in the medium. The final yield of .beta.-carotene is 17 g/L. **7235-40-7P**, .beta.-Carotene RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation) (prodn. of .beta.-carotene from Blakeslea trispora) ICM C12P023-00 IC 16-2 (Fermentation and Bioindustrial Chemistry) CC ST Blakeslea beta carotene fermn foam control IT Fermentation (fed-batch; prodn. of .beta.-carotene from Blakeslea trispora) IT Agitation (mechanical) Blakeslea trispora Foaming (prodn. of .beta.-carotene from Blakeslea trispora) IT **7235-40-7P**, .beta.-Carotene RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation) (prodn. of .beta.-carotene from Blakeslea trispora) IT 1338-39-2, Span 20 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (prodn. of .beta.-carotene from Blakeslea trispora)

L81 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:215496 HCAPLUS

DOCUMENT NUMBER: 120:215496

Fermentative manufacture of .beta.-carotene. TITLE: INVENTOR(S): Matsumura, Shigeo; Sumino, Yasuhiro; Matsui, Junji PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan SOURCE: Eur. Pat. Appl., 12 pp. CODEN: EPXXDW DOCUMENT TYPE: Patent LANGUAGE: English FAMILY ACC. NUM. COUNT: PATENT INFORMATION: PATENT NO. APPLICATION NO. DATE KIND DATE EP 586255 A1 19940309 EP 1993-306964 19930902 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE CA 1993-2105527 19930903 AA 19940304 CA 2105527 JP 06153986 A2 19940603 JP 1993-219427 19930903 PRIORITY APPLN. INFO.: JP 1992-236176 19920903 .beta.-Carotene is manufd. using a microalga tolerant to an active O generator, such as methylene blue and rose bengal, and capable of producing .beta.-carotene. The microalga is preferably Chlorella pyrenoidosa. IT **7235-40-7P**, .beta.-Carotene RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation) (manuf. of, fermentative, with Chlorella pyrenoidosa) 7782-44-7, Oxygen, biological studies TT RL: BIOL (Biological study) (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa) IC ICM C12P023-00 ICS C12N001-12 C12P023-00, C12R001-89 ICI 16-8 (Fermentation and Bioindustrial Chemistry) CCST fermn Chlorella beta carotene IT Chlorella pyrenoidosa (.beta.-carotene manuf. by fermn. with) TT Fermentation (.beta.-carotene, with Chlorella pyrenoidosa) 61-73-4, Methylene blue 11121-48-5, Rose bengal IT RL: BIOL (Biological study) (in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa) IT **7235-40-7P**, .beta.-Carotene RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation) (manuf. of, fermentative, with Chlorella pyrenoidosa) 7782-44-7, Oxygen, biological studies TT RL: BIOL (Biological study) (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa) => d ibib abs 13-17 L81 ANSWER 13 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN ACCESSION NUMBER: 1998-467550 [40] WPIX DOC. NO. CPI: C1998-141821 TITLE: Fermentative production of valuable compound(s) - by fermentation of a microbial strain on an industrial scale using a chemically **defined** medium and recovery of the compound(s).

DERWENT CLASS:

B04 D16

INVENTOR(S):

DE LAAT, W T A; KOEKMAN, B P; PREUSTING, J C G; DE LAAT,

WTAM

PATENT ASSIGNEE(S):

(KONN) GIST-BROCADES BV; (STAM) DSM NV; (DLAA-I) DE LAAT W T A M; (KOEK-I) KOEKMAN B P; (PREU-I) PREUSTING J C G .

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK PG LA

WO 9837179 A2 19980827 (199840)* EN 37

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA

PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG

US UZ VN YU ZW

A 19980909 (199905) AU 9864000

EP 970236. A2 20000112 (200008) EN

R: AL AT BE CH DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

A3 20000412 (200026) CZ 9902954

BR 9807362 A 20000418 (200032)

A 20000322 (200032) CN 1248294

KR 2000075487 A 20001215 (200131)

A1 20000601 (200133) MX 9907691

JP 2001512970 W 20010828 (200156) 44

US 2002039758 A1 20020404 (200227)

APPLICATION DETAILS: .

PA	TENT NO K	IND ·	APPLICATION	DATE
WO	9837179	A2 ·	WO 1998-EP1122	19980220
ΑU	9864000	Α	AU 1998-64000	19980220
EΡ	970236 ⁻	A2	EP 1998-909483	19980220
			WO 1998-EP1122	19980220
CZ	9902954	A3	WO 1998-EP1122	19980220
			CZ 1999-2954	19980220
BR	9807362	Α	BR 1998-7362	19980220
			WO 1998-EP1122	19980220
CN	1248294	. A	CN 1998-802632	19980220
KR	2000075487	Α	WO 1998-EP1122	19980220
			KR 1999-707546	19990819
MX	9907691	A1	MX 1999-7691	19990819
JΡ	2001512970	W	JP 1998-536284	19980220
			WO 1998-EP1122	19980220
ŲS	2002039758	A1 Div ex	US 1999-367029	19991025
			US 2001-982474	20011017

FILING DETAILS:

PATENT NO	KIND	Ρ.	ATENT NO
AU 9864000	A Based	on W	0 9837179
EP 970236	A2 Based	on W	0 9837179
CZ 9902954	A3 Based	on W	0 9837179
BR 9807362	A Based	on W	0 9837179
KR 200007548	87 A Based	on W	0 9837179
JP 20015129	70 W Based	on W	0 9837179

PRIORITY APPLN. INFO: EP 1997-200494 19970220

AN 1998-467550 [40] WPIX

AB WO 9837179 A UPAB: 19981008

A process for the production of a valuable compound comprises: (a) fermentation of a micr bial strain of an industrial

fermentation of a micr bial strain of an industrial scale in a fermentation medium which is a chemically defined

medium composed of chemically defined constituents; and (b) recovery of

the valuable compound from the fermentation broth.

Also claimed is a method for preparing and/or improving a microbial strain producing a valuable compound of interest which is capable of being fermented on an industrial scale in a chemically defined medium, comprising: (a) subjecting a suitable parent strain to a mutagenic treatment selected from physical mutagens and chemical mutagens, and/or to DNA transformation; (b) screening the resulting mutants and/or transformants for their growth performance on a chemically defined medium and their production level of the valuable compound of interest; (c) selecting mutants and/or transformants which have a good growth performance on a chemically defined medium and/or an improved production level of the valuable compound of interest as compared to the parent strain.

USE - The method can be used for the production of valuable compounds such as beta-lactam compounds, enzymes, astaxanthin, arachidonic acid, triglycerides, beta-carotene, glucose isomerase (GI), clavulanic acid or erythromycin (claimed).

ADVANTAGE - The productivity of microbial strains in chemically defined media, when measured on an industrial scale, may be comparable to or in some cases even higher than their productivity in complex media. Oxygen transfer from the gas phase to the liquid phase and the carbon dioxide transfer from the liquid phase to the gas phase is improved substantially as compared to using complex media. The use of chemically defined media has a favourable influence on morphology, i.e. by producing a more rigid pellet which does not easily fall apart during fermentation. In addition, the chemically defined medium can decrease the viscosity of filamentous fermentation broths and improve downstream processing.

Dwg.0/2

L81 ANSWER 14 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER:

1995-053688 [08] WPIX

DOC. NO. CPI:

C1995-024479

TITLE:

New bacteria which produce carotenoid pigments

- used for the prodn. of astaxanthin, adonixanthin, beta-

carotene, echinenone, canthaxanthin and

zeaxanthin.

DERWENT CLASS:

BO4 BO5 D13 D16 D21 E24

INVENTOR(S):

KIYOTA, T; TAKAKI, M; TSUBOKURA, A; YONEDA, H

PATENT ASSIGNEE(S):

(NIOC) NIPPON OIL KK; (MISQ) NIPPON MITSUBISHI OIL CORP; (NIOC) NIPPON OIL CO LTD; (NIOC) NIPPON MITSUBISHI OIL

CORP

COUNTRY COUNT:

9

PATENT INFORMATION:

PATENT	NO	KIND	DATE	WEEK	LA	PG
EP 635	576	A1	19950125	(199508)*	EN	29
R:	CH DE	FR (GB LI			
NO 9402	2731	Α	19950123	(199511)		
CA 2128	8549	. A	19950123	(199516)		
JP 070	79796	Α	19950328	(199521)		20

US	5607839	Α	19970304	(199715)		16
US	5858761	Α	19990112	(199910)		
EΡ	635576	B1	20000830	(200042)	EN	
	R: CH DE	FR (GB LI			
DE	69425706	Ε	20001005	(200057)		
JΡ	3242531	B2	20011225	(200203)		20
NO	313204	R1	20020826	(200263)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 635576	A1	EP 1994-111525	19940722
NO 9402731	Α	NO 1994-2731	19940721
CA 2128549	Α .	CA 1994-2128549	19940721
JP 07079796	Α	JP 1994-152240	19940704
US 5607839	Α	US 1994-276943	19940719
US 5858761	A Div ex	US 1994-276943	19940719
		US 1996-716841	19960919
EP 635576	B1	EP 1994-111525	19940722
DE 69425706	E	DE 1994-625706	19940722
		EP 1994-111525	19940722
JP 3242531	B2	JP 1994-152240	19940704
NO 313204	B1	NO 1994-2731	19940721

FILING DETAILS:

US 5858761 A Div ex US 5607839 DE 69425706 E Based on EP 635576	
JP 3242531 B2 Previous Publ. JP 07079796 NO 313204 B1 Previous Publ. NO 9402731	5

PRIORITY APPLN. INFO: JP 1993-181615 19930722

AN 1995-053688 [08] WPIX

AB EP 635576 A UPAB: 19950301

Bacteria belonging to a new genus and having the following properties are claimed: (1) morphology: polymorphic rod; (2) motility:motile; (3) flagella:peritrichous; (4) spore formation:none; (5) gram strain:negative; (6) prodn. of pigment:positive (water insoluble); (7) oxidase:positive; (8) catalase:positive; (9) behaviour toward oxygen:aerobic; (10) fermentation of glucose:negative; (11) prodn. of 3-ketolactose:negative; (12) quinone type:Q-10; (13) GC content of intracellular DNA:64-69 molar %; (14) formation of slime:glucose, negative; sucrose, negative; (15) presence of sphingolipid:negative; (16) presence of bacteriochlorophyll:negative.

USE - The bacteria can be cultured to produce one or a mixt. of carotenoid pigments selected from astaxanthin adonixanthin, beta-carotene, echinenone, canthaxanthin and zeaxanthin. The carotenoid pigments can be used as additives in food, feed, pharmaceuticals, cosmetics, etc.

ADVANTAGE - Using the bacteria, carotenoids can be produced on an industrial scale. They can produce natural type astaxanthin., Almost 100% of astaxanthin produced by the bacteria is (3S,3'S)-astaxanthin. Dwg.0/6

ABEQ US 5607839 A UPAB: 19970410

A new process for production of a **carotenoid** pigment selected from the group consisting of astaxanthin, adonixanthin, beta**carotene**, echinenone, canthaxanthin, zeaxanthin and mixtures thereof, comprising the steps of:

culturing bacterium strain E-396, FERM BP-4283, or A-581-1, FERM BP-4671, in an aqueous nutrient medium comprising sources of carbon, nitrogen, and inorganic substances and

recovering an individual carotenoid pigment or a mixture of the carotenoid pigments.

Dwg.0/6

L81 ANSWER 15 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER:

1991-369260 [50] WPIX

DOC. NO. CPI:

C1991-159215

TITLE:

Continuous fermentation of carotenoid

- producing microorganisms - by addn. of nutrient

at rate needed for max. growth.

DERWENT CLASS:

D13 D16 E24

INVENTOR(S):

BAILEY, R B; MEDWID, R D

B2 20000717 (200039)

PATENT ASSIGNEE(S):

(COOA) COORS BIOTECH INC; (ZEAG-N) ZEAGEN INC; (UVFO-N)

UNIVERSAL FOODS CORP; (ARCH) ARCHER-DANIELS MIDLAND CO

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA	PG							
WO 9118108	A 1991112	8 (199150)*	28							
RW: AT BE	CH DE DK ES	FR GB GR	IT LU	NL OA	SE						
W: AT AU	BB BG BR CA	CH DE DK	ES FI	GB HU	JP KP	KR	LK L	U MC	MW	NL	NO
'PL RO	SD SE SU										
AU 9180820	A 1991121	0 (199212))								
BR 9106448	A 1993051	8 (199324))								
EP 553085	A1 1993080	4 (199331) EN	28							
R: DE ES	FR GB GR IT	NL			•						
JP 06500008	W 1994010	6 (199406)	j	14							
EP 553085	A4 1993090	1 (199527))								
EP 553085	B1 1999102	0 (199948) EN								
R: DE ES	FR GB GR IT	NL									
DE 69131730	E 1999112	5 (200002))								
ES 2139577	T3 2000021	6 (200016)								

15

APPLICATION DETAILS:

JP 3065348

PA	ΓENT NO	KIND	APPLICATION	DATE
BR	9106448	Α	BR 1991-6448	19910514
EP	553085	A1	WO 1991-US3358 EP 1991-910886	19910514 19910514
1P	06500008	W	WO 1991-US3358 JP 1991-510821	19910514 19910514
			WO 1991-US3358	19910514
EP	553085	Α4	EP 1991-910886	
EP	553085	B1	EP 1991-910886	19910514
			WO 1991-US3358	19910514
DE	69131730	E	DE 1991-631730	19910514
			EP 1991-910886	19910514
			WO 1991-US3358	19910514
ES	2139577	T3	EP 1991-910886	19910514
JР	3065348	B2	JP 1991-510821	19910514
			WO 1991-US3358	19910514

FILING DETAILS:

PATENT NO	KIND	PATENT NO
BR 9106448 EP 553085	A' Based on Al Based on	WO 9118108 WO 9118108
JP 06500008	W Based on	WO 9118108
EP 553085 DE 69131730	B1 Based on E Based on	WO 9118108 EP 553085
ES 2139577	Based on T3 Based on	WO 9118108 EP 553085
JP 3065348	B2 Previous Pub Based on	7. JP 06500008 WO 9118108

PRIORITY APPLN. INFO: US 1990-524140 19900515

AN 1991-369260 [50] WPIX

AB WO 9118108 A UPAB: 19960108

A continuous fermentation method for carotenoid

-producing heterotrophic microorganisms is claimed comprising (a) diluting a **fermentation** broth comprising the microorganism by continuously adding fresh **fermentation** medium comprising a nutrient to the **fermentation** broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the **fermentation** broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species Neospongiococcum excentricum (ATCC40355). The nutrient is pref. glucose or sucrose. The fermentation broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO2 in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. @(28pp Dwg.No.0/0)
0/0

ABEQ EP 553085 A UPAB: 19931118

A continuous fermentation method for carotenoid -producing heterotrophic microorganisms is claimed comprising (a) diluting a fermentation broth comprising the microorganism by continuously adding fresh fermentation medium comprising a nutrient to the fermentation broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the fermentation broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species Neospongiococcum excentricum (ATCC40355). The nutrient is pref. glucose or sucrose. The fermentation broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO2 in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. Dwg.0/0

L81 ANSWER 16 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1974-80388V [46] WPIX

TITLE: Deep culturing microorganisms with adequate

oxygen - stirring rate and

oxygen flow adjusted to secure full

xygen access.

DERWENT CLASS:

D16

PATENT ASSIGNEE(S):

(KRIK-N) KIRKHENSHTEIN MICROBIOL

COUNTRY COUNT:

1

PATENT INFORMATION:

PRIORITY APPLN. INFO: SU 1971-1684597 19710727

AN 1974-80388V [46] WPIX

AB SU 413183 A UPAB: 19930831

In the title **culturing** when thre air input is 0.3-3.0 vols/vol. medium per min., the stirring rate is increased in steps, and when the exit gas inhibiting CO2 concn. is 3-11% the stirring rate is cut stepwise with increase also in air supply. In the case of the lysin producer Brevibacterium sp. 22, at an air speed 1.2 vols/vol. medium/per min., the stirring rate steps are 180, 230, 280, 330, 380 r.p.m., and when the exit gas CO2 conc. is 4% the stirrer speed sequence is reversed. With the **carotenoid producer** Rhodotorula gracilis Mn, using an air input of 2.0 vols./vol./min., the stirring speeds are 200, 300, 400 r.p.m., then with 11% CO2 in the exit gas the sequence is reversed.

L81 ANSWER 17 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER:

1972-39521T [25] WPIX

TITLE:

Carotenoid contg concentrates -

microbiological prodn.

DERWENT CLASS:

B04 D16

PATENT ASSIGNEE(S):

(KIR-N) INST MIKROBIOLOGII IM AUG

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 2059387	Α		(197225)*		
GB 1293995	Α		(197243)		
FR 2117801	Α		(197246)		
JP 49004386	В	19740131	(197409)		

PRIORITY APPLN. INFO: DE 1970-2059387 19701202

AN 1972-39521T [25] WPIX

AB DE 2059387 A UPAB: 19930831

Carotenoid-contg. concentrates useful in the prodn. of fodder prods. and in the food and medicinal inds. are produced by cultivating carotenoid-producing micro-organisms under aerobic conditions on a nutrient medium contg. sources of C, N, mineral salts, biologically active substances, stimulants and carotenoid precursors until maximal accumulation of the biomass in the fermentation medium, effecting a partial separation of the fermentation medium from the biomass to give a biomass conc. of is not <50 g (dry wt) per litre of medium, and accumulating carotenoid by maintaining the concentrate (optionally after adding carbohydrate and/or trace elements) at 28-35 degrees C and pH 5-7 while aerating at a rate of 80-150 mg

O2/litre/minute. Fermentati n time is shortened energy requirements are reduced, and the capacity and amt. of equipment required are less

=> file home FILE 'HOME' ENTERED AT 12:10:41 ON 28 JUL 2003

Inventor Search

MARX 09/049,228

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=> d his

(FILE 'HOME' ENTE
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(FILE 'HOME' ENTERED AT 10:50:39 ON 28 JUL 2003)

FILE 'HCAPLUS' ENTERED AT 10:50:50 ON 28 JUL 2003.

L1 19 S TSUBOKURA A?/AU

L2 337 S MIZUTA H?/AU

L3 354 S L1-2

L4 8 S L3 AND CAROTENOID SELECT RN L4 1-8

FILE 'REGISTRY' ENTERED AT 10:51:40 ON 28 JUL 2003 L5 42 S E1-42 SAVE TEMP L5 MAR228INV/A

FILE 'HCAPLUS' ENTERED AT 10:51:59 ON 28 JUL 2003

L6 5 S L4 AND L5

16 5 S L4 AND L5 17 8 S L4 OR L6 8 cites of 42 cpds displayed

=> d ibib abs hitstr ind 1-8

L7 ANSWER 1 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:924027 HCAPLUS

DOCUMENT NUMBER: 136:52783

TITLE: Process for producing carotenoid pigments

INVENTOR(S): Tsubokura, Akira; Mizuta, Haruyoshi

PATENT ASSIGNEE(S): Nippon Mitsubishi Oil Corporation, Japan

SOURCE: PCT Int. Appl., 23 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent lananes

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND DATE	APPLICATION NO.	DATE
WO 2001096591	A1 200112 CN, IL, KR, U		20010608
	CH, CY, DE, D	K, ES, FI, FR, GB, GR, IE	, IT, LU, MC, NL,
JP 2001352995	A2 200112		20000612 20010608
.	A1 200208	07 EP 2001-936932	20010608
R: AT, BE, IE, FI,	• •	S, FR, GB, GR, IT, LI, LU	, NL, SE, MC, PT,
US 2003044886			20020211
PRIORITY APPLN. INFO	. :	JP 2000-175124 A WO 2001-JP4874 W	20010608

AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given. The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a lig. culture medium during the fermn.

IT 382660-64-2 382660-65-3

RL: PRP (Properties)

(nucleotide sequence; process for producing carotenoid pigments) RN 382660-64-2 HCAPLUS

CN DNA (bacteria strain E-396 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 382660-65-3 HCAPLUS

CN DNA (bacteria strain A-581-1 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone

472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone

4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin

7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)

(process for producing carotenoid pigments)

RN 144-68-3 HCAPLUS

CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 432-68-8 HCAPLUS

CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

RN 472-61-7 HCAPLUS CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 472-70-8 HCAPLUS CN .beta.,.beta.-Caroten-3-ol, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry. Double bond geometry as shown.

RN 514-78-3 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond géometry as shown.

PAGE 1-A

PAGE 1-B

RN 4339-77-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

RN 4418-72-8 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-73-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

RN 7235-40-7 HCAPLUS

CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-B

RN 7782-44-7 HCAPLUS

CN Oxygen (8CI, 9CI) (CA INDEX NAME)

0 = 0

IC ICM C12P023-00

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST carotenoid manuf bacteria dissolved oxygen

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study) (16 S, gene for; process for producing carotenoid pigments)

IT Bacteria (Eubacteria)

Culture media

DNA sequences

Fermentation

Taxonomy

(process for producing carotenoid pigments)

IT Carotenes, preparation

RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP

(Preparation)

(process for producing car tenoid pigments)

IT Gene, microbial

```
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (process for producing carotenoid pigments)
    382660-64-2 382660-65-3
IT.
     RL: PRP (Properties)
        (nucleotide sequence; process for producing carotenoid
     144-68-3P, Zeaxanthin 432-68-8P, Echinenone
IT
     472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
     514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
     4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
     7235-40-7P, .beta.-Carotene
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (process for producing carotenoid pigments)
     7782-44-7, Oxygen, biological studies
IT
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (process for producing carotenoid pigments)
                               THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
                         12
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
L7
                         2001:251697 HCAPLUS
ACCESSION NUMBER:
                         134:294933
DOCUMENT NUMBER:
                         Bacterial carotenoid-containing preparations
TITLE:
                         as feed additive
                         Tsubokura, Akira; Yoneda, Hisashi; Mizuta,
INVENTOR(S):
                         Yoshinori
                         Nisseki Mitsubishi K. K., Japan
PATENT ASSIGNEE(S):
                         Jpn. Kokai Tokkyo Koho, 6 pp.
SOURCE:
                         CODEN: JKXXAF
DOCUMENT TYPE:
                         Patent
LANGUAGE:
                         Japanese
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                                           APPLICATION NO. DATE
                      KIND DATE
                       A2
                            20010410
                                           JP 1999-279337
                                                            19990930
     JP 2001095500
                            20010711
                                           NO 2001-2629
                                                            20010529
     NO 2001002629
                       Α
PRIORITY APPLN. INFO.:
                                        JP 1999-279337
                                                         A 19990930
                                        WO 2000-JP6528
     The prepns. comprise ppt. of microbial culture contg. .gtoreq.3%
AB
     carotenoids with astaxanthin content preferably .gtoreq.40%. The
     microbes are preferably those which contain 16 S rRNA-specifying DNA
     having sequence substantially homologous to 1452-bp sequence (given).
     carotenoids are stable to O and light because they are stabilized
     with cell membrane and cell wall. E-396 (FERM BP-4283) was cultured in a
     medium contg. yeast ext., peptone, glucose, and salts at 28.degree. for 6
            The collected cells was dried to give a pigment prepn. (total
     carotenoids 31.2%) contg. .beta.-carotene 1.6, echinenone 1.9,
     3-hydroxyechinenone 0.9, canthaxanthin 2.3, adonirubin 5.6, astaxanthin
     13.0, asteroidenone 0.6, adonixanthin 5.3, and zeaxanthin 0.01%.
     144-68-3P, Zeaxanthin 432-68-8P, Echinenone
     472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin
     4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin
     4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
     19866-02-5P, Asteroidenone
     RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD
     (Food or feed use); BIOL (Biological study); PREP (Preparation); USES
```

(Uses)

(manuf. of astaxanthin-rich car tenoid-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

144-68-3 HCAPLUS RN

.beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME) CN

Absolute stereochemistry. Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 432-68-8 HCAPLUS

.beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME) CN

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

472-61-7 HCAPLUS

RN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA CN INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 514-78-3 HCAPLUS CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4339-77-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-72-8 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-73-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 7235-40-7 HCAPLUS

CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 19866-02-5 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 7,8-didehydro-3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

IT 334071-56-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)

(manuf. of astaxanthin-rich carotenoid-contg. prepns. for

feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

RN 334071-56-6 HCAPLUS

CN DNA (bacteria strain E-396 16 S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM A23K001-16

ICS C09B061-00; C09B067-20; C12N001-20

CC 17-12 (Food and Feed Chemistry)

Section cross-reference(s): 16, 18

ST astaxanthin rich carotenoid contg microbial culture feed additive

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study) (16 S, DNA for; manuf. of astaxanthin-rich carotenoid-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Bacteria (Eubacteria)

(E-396; manuf. of astaxanthin-rich carotenoid-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Feed additives

Fermentation

Pigments, biological

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Carotenes, biological studies

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(manuf. of astaxanthin-rich carotenoid-contg. prepns. for

```
feed with microorganisms having specific 16 S rRNA-specifying DNA
        sequence)
     DNA
IT
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (manuf. of astaxanthin-rich carotenoid-contg. prepns. for
        feed with microorganisms having specific 16 S rRNA-specifying DNA
        sequence)
     144-68-3P, Zeaxanthin 432-68-8P, Echinenone 472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin
IT
     4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
     19866-02-5P, Asteroidenone
     RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD
     (Food or feed use); BIOL (Biological study); PREP (Preparation); USES
     (Uses)
        (manuf. of astaxanthin-rich carotenoid-contg. prepns. for
        feed with microorganisms having specific 16 S rRNA-specifying DNA
        sequence)
     334071-56-6
IT
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (manuf. of astaxanthin-rich carotenoid-contg. prepns. for
        feed with microorganisms having specific 16 S rRNA-specifying DNA
        sequence)
     ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
L7
ACCESSION NUMBER:
                          1999:85961 HCAPLUS
DOCUMENT NUMBER:
                          130:279042
                          Paracoccus carotinifaciens sp. nov., a new aerobic
TITLE:
                          gram-negative astaxanthin-producing bacterium
AUTHOR(S):
                          Tsubokura, Akira; Yoneda, Hisashi;
                          Mizuta. Haruyoshi
                          Central Technical Research Laboratory, Nippon Oil
CORPORATE SOURCE:
                          Company Ltd, Yokohama, 231-0815, Japan
                          International Journal of Systematic Bacteriology
SOURCE:
                          (1999), 49(1), 277-282
                          CODEN: IJSBA8; ISSN: 0020-7713
                          Society for General Microbiology
PUBLISHER:
DOCUMENT TYPE:
                          Journal
LANGUAGE:
                          English
     The strain E-396T, isolated from soil, was Gram-neg., aerobic,
     orange-pigmented, rod-shaped, motile by peritrichous flagella and
     astaxanthin-producing. This organism produced carotenoids.
     mainly astaxanthin, and did not produce bacteriochlorophyll.
     ubiquinone system was Q-10. Anal. of the 16S rRNA sequence of strain
     E-396T showed it to be a member of the .alpha.-3 subclass of the
     Proteobacteria, forming a cluster with the species of the genus
     Paracoccus. On the basis of the prodn. of orange pigments and motility by
     peritrichous flagella, together with DNA-DNA reassocn. data, it is
     concluded that the new isolate should be classified into a new species of
     the genus Paracoccus, Paracoccus carotinifaciens sp. nov. The type strain
     is E-396T ( = IFO 16121T).
     472-61-7, Astaxanthin
IT
     RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL
     (Biological study); FORM (Formation, nonpreparative)
        (Paracoccus carotinifaciens sp. nov., new aerobic gram-neg.
        astaxanthin-producing bacterium)
     472-61-7 HCAPLUS
RN
     .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA
CN
```

INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

IT 222713-29-3

RL: PRP (Properties)

(nucleotide sequence; Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

RN 222713-29-3 HCAPLUS

CN DNA (Paracoccus carotinifaciens strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

Section cross-reference(s): 3
ST Paracoccus carotinifaciens 16S rRNA gene sequence taxonomy

IT rRNA

RL: PRP (Properties)

(16 S; Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT DNA sequences

Evolution

Paracoccus carotinifaciens

Taxonomy

(Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT Gene, microbial

RL: PRP (Properties)

(for 16S rRNA; Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT 472-61-7, Astaxanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

MARX 09/049,228

(Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium) IT 222713-29-3 RL: PRP (Properties) (nucleotide sequence; Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium) REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN L7 1997:772393 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 128:59314 Carotenoid-stabilization material TITLE: INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Uchiyama, Yoko; Mizuta, Yoshitaka PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan Jpn. Kokai Tokkyo Koho, 14 pp. SOURCE: CODEN: JKXXAF DOCUMENT TYPE: Patent LANGUAGE: Japanese FAMILY ACC. NUM. COUNT: 1 PATENT INFORMATION: PATENT NO. KIND DATE APPLICATION NO. DATE JP 09308481 A2 19971202 JP 1996-128565 19960523 JP 3278574 **B2** 20020430 PRIORITY APPLN. INFO.: JP 1996-128565 19960523 The title material (I) is produced by microorganism E-396 or mutant microorganism A-581-1. I is useful for improvement/stabilization of meat. egg, and/or skin color. Physiol, and morphol, characteristics of the microorganism E-396 were given. ICM C12N001-20 IC ICS A23K001-16; A23K001-18; A23L001-272; C09B061-00; C12N015-09; C12Q001-68; C12N001-20; C12R001-01 CC 10-1 (Microbial, Algal, and Fungal Biochemistry) Section cross-reference(s): 16, 17 ST carotenoid stabilization material microorganism fermn IT Aquaculture Egg, poultry Feed additives Fermentation Food additives Health food Meat Microorganism (carotenoid-stabilization material) IT Carotenes, biological studies RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (carotenoid-stabilization material) ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN L7 1996:338419 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 125:9229 TITLE: Process for extraction of carotenoids from bacterial cells Kitaoka, Motomitsu; Tsubokura, Akira; INVENTOR(S): Kiyota, Takashi

Nippon Oil Company, Ltd., Japan

PATENT ASSIGNEE(S):

SOURCE:

Can. Pat. Appl., 10 pp.

CODEN: CPXXEB

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2159176	AA	19960328	CA 1995-2159176	19950926
JP 08089280	A2	19960409	JP 1994-231266	19940927
US 5591343	Α	19970107	US 1995-533390	19950925
NO 9503813	Α	19960328	NO 1995-3813	19950926
EP 719866	A1	19960703	EP 1995-306770	19950926
EP 719866	B1	20011205		

R: CH, DE, FR, GB, LI

PRIORITY APPLN. INFO.:

JP 1994-231266 A 19940927

A process for extn. of a carotenoid compd. from bacterial cells contg. the carotenoid compd. comprising the step of bringing the bacterial cells into contact with supercrit. fluid to ext. the carotenoid compd. from the cells. The process provides carotenoid compds. which can be safely used as feed additives and food additives.

IC ICM C07C403-00 ICS C07C011-21

17-14 (Food and Feed Chemistry)

process extn carotenoid bacterial cell ST

IT Feed

Food

(additives; process for extn. of carotenoids from bacterial cells)

IT Bacteria

Extraction

(process for extn. of carotenoids from bacterial cells)

Carotenes and Carotenoids, biological studies IT RL: FFD (Food or feed use); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); USES (Uses)

(process for extn. of carotenoids from bacterial cells)

IT Fluids

(supercrit., process for extn. of carotenoids from bacterial cells)

ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN 17

ACCESSION NUMBER:

1996:153672 HCAPLUS

DOCUMENT NUMBER:

124:198044

TITLE:

Novel bacteria producing carotenoids

INVENTOR(S):

Tsubokura, Akira; Yoneda, Hisashi; Takagi,

Mikihiro; Kyota, Takashi Nippon Oil Co Ltd, Japan

PATENT ASSIGNEE(S): SOURCE:

Jpn. Kokai Tokkyo Koho, 20 pp.

CODEN: JKXXAF

DOCUMENT TYPE:

Patent

LANGUAGE:

Japanese

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 08009964	A2	19960116	JP 1994-152078	19940704
JP 3429563	B2	20030722		,

MARX 09/049,228

```
PRIORITY APPLN. INFO.:
                                        JP 1994-152078
                                                            19940704
    Two novel bacteria capable of producing car tenoids are isolated
     and characterized. FERM BP-4283 strain E-396 and FERM BP-4671 strain
     A-581-1 are both aerobic, gram-neg. bacteria. A phylogenetic tree of the
     bacteria is also provided.
IC
     ICM C12N001-20
    C12P023-00
ICA
ICI
    C12N001-20, C12R001-01; C12P023-00, C12R001-01
     10-1 (Microbial, Algal, and Fungal Biochemistry)
CC
ST
     bacteria carotenoid prodn
IT
     Bacteria
        (FERM BP-4283 strain E-396, FERM BP-4671 strain A-581-1; isolation of
        novel bacteria producing carotenoids)
IT
     Carotenes and Carotenoids, preparation
     RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
     (Preparation)
        (isolation of novel bacteria producing carotenoids)
    ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                         1995:849314 HCAPLUS
DOCUMENT NUMBER:
                         123:254690
TITLE:
                         Process for extracting carotenoids
                         Kitaoka, Motomitsu; Tsubokura, Akira;
Kiyota, Takashi
INVENTOR(S):
                         Nippon Oil Co. Ltd., Japan
PATENT ASSIGNEE(S):
                         Eur. Pat. Appl., 10 pp.
SOURCE:
                         CODEN: EPXXDW
DOCUMENT TYPE:
                         Patent
                         English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                                           APPLICATION NO.
                      KIND DATE
                                                            DATE
     -----
     EP 670306
                      A1
                            19950906
                                           EP 1995-102933
                                                            19950302
        R: CH, DE, FR, GB, LI
     JP 07242621
                     A2
                                           JP 1994-32388
                            19950919
                                                            19940302
     CA '2143689
                       AA
                            19950903
                                           CA 1995-2143689 19950301
     NO 9500804
                            19950904
                                           NO 1995-804
                       Α
                                                            19950301
PRIORITY APPLN. INFO.:
                                        JP 1994-32388
                                                            19940302
    A process for extg. carotenoid compds. comprising the step of
     bringing a material contg. the carotenoid compd. into contact
     with a cyclic hydrophilic org. compd. to ext. the carotenoid
     compd. from the material to the cyclic hydrophilic org. compd. By this
     process, a carotenoid compd. can be efficiently extd. resulting
     in an ext. contg. a high concn. of the carotenoid compd.
     116-30-3P 144-68-3P, Zeaxanthin 432-68-8P,
    Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P,
     Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P,
     .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P,
     Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P
     , Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P,
     .beta.-Carotene
     RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL
     (Biological study); PREP (Preparation)
        (extg. carotenoids)
     116-30-3 HCAPLUS
RN
     4,5'-retro-.beta.,.beta.-Carotene-3,3'-dione, 4',5'-didehydro- (9CI) (CA
CN
     INDEX NAME)
```

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 144-68-3 HCAPLUS CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 432-68-8 HCAPLUS

CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 432-70-2 HCAPLUS

CN .beta.,.epsilon.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 472-61-7 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 472-70-8 HCAPLUS CN .beta.,.beta.-Caroten-3-o1, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 472-93-5 HCAPLUS

CN .beta.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 502-65-8 HCAPLUS

CN .psi.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 514-78-3 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4339-77-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-72-8 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-73-9 HCAPLUS CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry. Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 7235-40-7 HCAPLUS CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A

IT 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, uses RL: NUU (Other use, unclassified); USES (Uses) (extg. carotenoids)

Ethane, 1,1'-oxybis- (9CI) (CA INDEX NAME)

H₃C-- CH₂-- O-- CH₂-- CH₃

RN 64-17-5 HCAPLUS CN Ethanol (9CI) (CA INDEX NAME)

H₃C-- CH₂-- OH ⁻

CN

RN 67-56-1 HCAPLUS CN Methanol (8CI, 9CI) (CA INDEX NAME)

H₃C-OH

RN 67-64-1 HCAPLUS CN 2-Propanone (9CI) (CA INDEX NAME)

0 || H3C-- C-- CH3

RN 67-66-3 HCAPLUS CN Methane, trichloro- (9CI) (CA INDEX NAME)

RN 71-23-8 HCAPLUS CN 1-Propanol (9CI) (CA INDEX NAME)

H₃C-CH₂-CH₂-OH

RN 71-43-2 HCAPLUS CN Benzene (8CI, 9CI) (CA INDEX NAME)



RN 75-09-2 HCAPLUS CN Methane, dichloro- (8CI, 9CI) (CA INDEX NAME)

C1-CH2-C1

RN 78-93-3 HCAPLUS CN 2-Butanone (8CI, 9CI) (CA INDEX NAME)

RN 108-20-3 HCAPLUS CN Propane, 2,2'-oxybis- (9CI) (CA INDEX NAME)

i-Pr-0-Pr-i

RN 108-88-3 HCAPLUS CN Benzene, methyl- (9CI) (CA INDEX NAME)

RN 108-94-1 HCAPLUS CN Cyclohexanone (7CI, 8CI, 9CI) (CA INDEX NAME)

RN 109-99-9 HCAPLUS CN Furan, tetrahydro- (7CI, 8CI, 9CI) (CA INDEX NAME)

0

RN 110-54-3 HCAPLUS CN Hexane (8CI, 9CI) (CA INDEX NAME)

Me-(CH₂)₄-Me

RN 110-82-7 HCAPLUS CN Cyclohexane (8CI, 9CI) (CA INDEX NAME)



RN 110-86-1 HCAPLUS CN Pyridine (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 123-86-4 HCAPLUS CN Acetic acid, butyl ester (8CI, 9CI) (CA INDEX NAME)

n-Bu-O-Ac

RN 123-91-1 HCAPLUS CN 1,4-Dioxane (9CI) (CA INDEX NAME)



RN 141-78-6 HCAPLUS CN Acetic acid ethyl ester (8CI, 9CI) (CA INDEX NAME)

```
Et-0-Ac
RN
     142-82-5 HCAPLUS
CN
     Heptane (8CI, 9CI) (CA INDEX NAME)
Me-(CH<sub>2</sub>)<sub>5</sub>-Me
RN
     563-80-4 HCAPLUS
     2-Butanone, 3-methyl- (8CI, 9CI) (CA INDEX NAME)
CN
RN
     1330-20-7 HCAPLUS
     Benzene, dimethyl- (9CI) (CA INDEX NAME)
CN
2 (D1-Me)
     ICM C07C403-24
     ICS C12P023-00
CC
     16-1 (Fermentation and Bioindustrial Chemistry)
ST
     carotenoid fermn extn
     Algae
     Bacteria
     Corynebacterium .
     Dunaliella
     Fermentation
     Haematococcus pluvialis
     Phaffia rhodozyma
        (carotenoid extn. from)
     Carotenes and Carotenoids, preparation
     RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL
     (Biological study); PREP (Preparation)
        (extg. carotenoids)
IT
     Ligroine
     RL: NUU (Other use, unclassified); USES (Uses)
         (extq. carotenoids)
     116-30-3P 144-68-3P, Zeaxanthin 432-68-8P,
IT
     Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P, Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P,
     .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P,
     Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P
      , Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P,
```

.beta.-Carotene

MARX 09/049,228

RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation) (extq. carotenoids) 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses IT 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, RL: NUU (Other use, unclassified); USES (Uses) (extg. carotenoids) ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN L7 ACCESSION NUMBER: 1995:489962 HCAPLUS DOCUMENT NUMBER: 122:289068 TITLE: Bacteria belonging to new genus and process for production of carotenoids using same. Tsubokura, Akira; Yoneda, Hisashi; Takaki, Mikihiro; Kiyota, Takashi INVENTOR(S): PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan Eur. Pat. Appl., 29 pp. SOURCE: CODEN: EPXXDW DOCUMENT TYPE: Patent English LANGUAGE: FAMILY ACC. NUM. COUNT: PATENT INFORMATION: PATENT NO. KIND DATE APPLICATION NO. DATE EP 635576 19950125 **A1** EP 1994-111525 19940722 EP 635576 **B1** 20000830 R: CH, DE, FR, GB, LI JP 07079796 19950328 JP 1994-152240 19940704 Α2 JP 3242531 B2 20011225 US 5607839 19970304 US 1994-276943 19940719 Α AA 19950123 CA 1994-2128549 19940721 CA 2128549 NO 9402731 Α 19950123 NO 1994-2731 19940721 US 5858761 Α 19990112 US 1996-716841 19960919 JP 1993-181615 PRIORITY APPLN. INFO.: A 19930722 US 1994-276943 A3 19940719 Bacterium belonging to a new genus, and a process for prodn. of carotenoid pigment selected from the group consisting of astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin and zeaxanthin, comprising the steps of culturing a bacterium capable of

carotenoid pigment selected from the group consisting of astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin and zeaxanthin, comprising the steps of culturing a bacterium capable of producing at least one of the carotenoid pigments, and recovering an individual carotenoid pigments. The producer bacterium belongs to new genus. According to the present process various carotenoids can be produced in an industrial scale. By the present process (3S, 3'S)-astaxanthin can be produced in an almost 100% purity.

IT 472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative) (bacteria belonging to new genus and process for prodn. of

carotenoids using same)

RN 472-61-7 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry. Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

RN 4418-73-9 HCAPLUS CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry. Double bond geometry as shown.

PAGE 1-A

PAGE 1-B

IT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process for prodn. of carotenoids using same)

RN 162875-45-8 HCAPLUS

CN DNA (bacterium strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM C12P025-00

ICS C12N001-20

16-5 (Fermentation and Bioindustrial Chemistry) CC

carotenoid formation bacteria; astaxanthin formation bacteria; adonixanthin formation bacteria; rRNA 16S gene sequence bacteria

IT Bacteria

Deoxyribonucleic acid sequences

(bacteria belonging to new genus and process for prodn. of carotenoids using same)

Carotenes and Carotenoids, biological studies ΙT

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL

(Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of carotenoids using same)

IT Gene, microbial

RL: PRP (Properties)

(bacteria belonging to new genus and process for prodn. of carotenoids using same)

IT Ribonucleic acids, ribosomal

RL: PRP (Properties)

(16 S, bacteria belonging to new genus and process for prodn. of carotenoids using same)

472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin ΙT

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL

(Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of carotenoids using same)

TT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process

for prodn. of carotenoids using same)

```
GenCore version 5.1.6
Copyright (d) 1993 - 2003 Compugen Ltd.
```

·:	
OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	July 28, 2003, 09:18:53; Search time 5293 Seconds (without alignments)
•	izzz. Jio militon cell updaces/sec
Title:	US-10-049-228-1 .
Periect score: Sequence:	1452 1 agtttgatcctggctcagaatgcggctggatcacctcctt 1452 ·
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0 Maximum DB seq length: 20	length: 0 length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database .	Gen Emb1:*

Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:* em_htgo_other:*

score greater than or equal to the score of the result being printed,	
peing	:10n.
result	l score distribution
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core o	total sc
the s	the to
ដ	oŧ
ednal	by analysis
ö	ana.
than	ρχ
greater	erived
re	1s
300	and is d

distribution.	2 t t C	11111111	06899 Paracoc	4/ Sequence	4,0	DNA encodi	ž	Š	<u>~</u>	74	AB008114 Paracoccu	5,5	69	20	99	15	6	75	200	200	7 7	0 0	60	73	92	8	2	200	9 6	2 0	86	58 1	08 Sequen	34 Pa	12	Paracoccus	87	74 Paracocc	Paracoccus	88 Paraco	74 Paracocc	15 Para				
score	3																							•																						
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Tsubokura,A., Yoneda,H., Takaki,M. and
Bacterial for production of carotenoids
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Tsubokura,A.
Tsubokura,A.
Direct Submission
Submitted (27-AuG-1997) Akira Tsubokura, Nippon Oil Company, Ltd.
Central Technical Research Laboratory; 8, Chidori-cho, Naka-ku,
Yokohama, Kanagawa 231, Japan (E-mail:a-tsubokura@nisseki.co.jp,
Tel:+81-45-625-7171, Fax:+81-45-625-7298)
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/mol_type="genomic DNA"
/strain="E-396"
/db_xref="taxon:65151"
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346 c 461 g 291 95500-A/1 :22553150 0-A/1. 0 1452) T 1452 T 1452

	136531 1452 bp DNA Sequence 1 from patent US 5607839. 136531. 136531.1 GI:2086356 Unknown. Unknown. Unknown. Unknown. Unknown. Unclassified. 1 (bases 1 to 1452)	Voneda, H., Takaki, M. Longing to new genus pr using same 5607839-A 1 04-MAR-1997 ation/Qualifiers 1452 346 c 461 g 291 99.9%; Score 1451;	Pred. No. 0; 0; daps 0; Mismatches 0; Indels 0; Gaps Accancercecececaccaccarcaccacca 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	61 GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGG 121 AATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGG 11111111111111111111111111111111111	Db	QY 361 GCGTGAGTGAAGGCCTTAGGGTTGTAAAGCTCTTCAGCTGGAAGATAATGACGGT 420 DD 111111111111111111111111111111111111
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AUTHORS TSUBORURA, A. and Mizuta, H.
A process for producing carotenoid pigments
TIȚLE A process for producing carotenoid pigments
Patent: WO 0196591-A 2 20-DEC-2001;
NIPPON MITSUBISHI OIL CORP, AKIRA TSUBOKURA, HARUYOSHI MIZU
ENT OS UNKNOWN
PN 20-DEC-2001
PF 08-20N-2001 WO 2001JP00A***
PR 12-JUN-2001 JP n^**
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                                AACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCT
                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
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Parabacteritum aurantiacum gen. nov., sp.
Astaxanthin producing marine bacteria
Unpublished
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                                                                                             /note="synonimous name given at accession:Agrobacterium aurantiacum~synonym:alpha proteobacterium MBIC1143"
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                  sp. MBIC1143*
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325 c 432 g 272 t
                                                                                                                                                                                                           Score 1344.8;
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0; Mismatches
1. .1360
/organism="Paracoccus sp./mol_type="genomic DNA"
/ration="Malcolid"
/isolate="Nallo"
/db_xref="taxon:81397"
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### TCAMACAACCCCCAAACCTTACCAACCCTTACAACCCAACAACA	TOGANGCANGGGGGAAACCTTACCAAGCCTTACACAGCAGGACCCTGGAAACTCC TGAAACCAAGCGGGAAACCTTACACACCTTACACCTGAAACCCTGAAACAACTC TGAAACCAAGCACCTCACACCCTTACACCTTGAACACCCTGAAAACTC TGAAACCAAGCACCTCACACCCTTACACCCTGAACACCCTGAAACTCCTGAAACTCCTGAAACTCCTACACCCTGAACACCCTGAAACTCCTGAACACCTCTCACACCCTGAACACCCTGAACACCTCTCACACCCTGAACACCTCTCACACCTTACATTCATT	tches 1374; Conservative 0; Mismatches 33; Indels 1; Gaps 1; tches 1374; Conservative 0; Mismatches 33; Indels 1; Gaps 1; 22 GAACGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	62 ATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGAGCAGTGGGG 32 1	TAACTCCGTGCCAGCAGCGCGGTAATACGGAGGGGCTAGCGTTGTCGGAATTACTGG TAACTCCGTGCCAGCCGCGGTAATACGGAGGGGCTAGCGTTGTTCGGAATTACTGG TAACTCCGTGCCAGCCGCGGTAATACGGAGGGGCTGAGCGTTGTTCGGAATTACTGG CGTAAAGCGCAGCGGACTGGAAGTTGGGGGGTGAAATCCCGGGCCTCAACCTTG CGTAAAGCGCAGCAGCGGACTGGAAGTTCGAGAGTGAAATCCCGGGCCTCAACCTTG CGTAAAAGCGCAGCAGGAAGTTCGAGAGAGGGGAAATCCCGAGTGTA 6 CAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGGAAATCCGAGTGTA 6 CAACTGCCTTCAAAACTATCGGAGGAACACCAGTGGGGAAGGGGGAATTCCGAGTGTA 6 CAACTGCAAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAAGGCGGCTCACTGGCTCGA 6 CAACTGCAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAAGGCGGCTCACTGGCTCGA 6 CAACTGCAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGCTCGA 6 CAACTGCAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTCACTCGACTCGA 6 CAACTGCAAATTCGTAGATATTCGGAAGAAGCGGCTCACTCGAAGGCCGAAAGGCGGCTCACTCGAAGGCCGAAAGGCGGCTCACTCGAAGGCCGCACTCGAAGGCCGAAAGGCCGCACTCGAAGGCCGAAACTCGCACCAGAAGCCGCACCAGAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAGAAGCCGCACCAC	1	GGCAGACCTTG AGAGACCTGCA AGTGACCTGTG AAGTCCGGCAA AAGTCCGGCAA AGTCCGGCAA AGTCCGGCAA
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	OY 61 GACCTTCGGGTCTAGCGGCGGACGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGG 120	OY 121 AATAGCCCCGGGAAACTGGGGGGAATACCGTATAGGCCCTTTGGGGGAAAGATTATCGG 180	QY 181 AGAAGGATCGGCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACG 240 .	OY 241 AICCATAGCIGGTITGAGAGGAIGAICACCACACTGGGACTGAGACACGGCCCAGACIC 300 1111111111111111111111111111111111	Qy 301 CTACGGGAGGCAGTGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCC 360	QY 361 GCGTGAGTGATGAGGCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGACGGT 420	Qy 421 ACCAGCAGAAGACCCCGGCTAACTCCGTGCCAGCAGCGGGTAATACGGAGGGGGCT 480 111111111111111111111111111111111111	Oy 481 AGCGTTGTTGGBATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTG 540	541	601 GTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGC 	661 GAAGGCGGCTCACTGCT 	721	GCAAGATTAA 8	782 ATTCGGTGACACCTAACGGATTAAGCATTCCGCCTGGGGGGTTACGGTCGCAAGATTAA 8	Qy 841 AACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGC 900	Qy 901 AACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGATTCAGCTTTCT 960 11	Qy 961 GTAAGAGACCTGCACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGGATGTTC 1020	OY 1021 GGTTAAGTCCGGCAACGAGCACCACGTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080 1022 GGTTAAGTCCGGCAACGAGCAACCCACGTCCCTAGTTGCCAGC-ATTCAGTTGGGCAC 1080	Qy 1081 TCTATGGAAACTGCCGATGATAAGTCGGAAGGTGTGGATGACGTCAAGTCCTCATGG 1140
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us-10-049-228-1.rge

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101 ACCARCTROGARTGCCTCTGGAACTGCAAGGGAAGAAGTGGAATGCAACTGCAAGGAATGCAATGCAAGTGCAAGTGAATGCGTCAAGTGCAACTGCAAGCAGAATGCGGCTCAAGAATGCGGCCTCAAGAATGCGGCCTCAAGAATGCGGCCTCAAGAATGCGTCCCAGAATGCATCCCGCCTCAAGAATGCGTCCCGTCAAGAATGCATCCCGCCTCAAGAATGCATCCCGCTCAAGAATGCATCCCGCCTCAAGAATGCATCCCGCTCAAGAATGCATCCCGCTCAAGAATGCATCCCGCTCAAGAATGCATCCCGTGAAATACTTCCCCGGGCTTTACACACAGAAGAACAACAAGAAGAAGAAGAAGAAGAAGAA	4 6 6 6 6 6 6	, dy	8 6 8 6 8 6 8	8 8 8 8 8	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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TO I OPO I DAG E ABOR E E EL MA	AGCCARCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA	AY014170 AY0141	Rhodobacteraceae; Paracoccus. I (bases I to 1461) Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G., Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G., Mitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G., Mayer,L.W., Rassoull,S.M., Barchet,W., Munro,C., Shuttleworth, and Bernard,R. Paracoccus yeeli sp. nov. (Formerly CDC Group EO-2), a Novel Bacterial Species Associated with Human Infection J. Clin. Microbiol. 41 (3), 1289-1294 (2003) 2 (bases I to 1461) Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., MacGregor,J., Steigerwalt,A.G. and Daneshvar,M.I.	Direct Summission Submitted (16-NOV-2000) NCID/DBMD/MSPB/SBRL, Centers for Disea Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, Location/Qualifiers 1. 1461 //organism="paracoccus yeeil" //mol_type="genomic DNA" //strain="G6155" //db_xref="taxon:147645" A	92.2%; Score 1338.6; DB 1; Length 1461; 6; Conservative 0; Mismatches 55; Indels 5; Gaps AGTITGATCCTGGCTCAGAACGAACGCTGGGGCAGGCTTAACACATGCAAGTCGAGCGA 60

184 AGGATCGGCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAACCA	304 CGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCCATGCCGCG 363 	364 TGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGTACC 423 	424 AGCAGAAGAAGCCCCGGGTAACTCCGTGCCAGCAGCGCGGGTAATACGGAGGGGGCTAGC 483 	484 GTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAA 543 	544 TCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGG 603 	604 AGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAA 663 	664 GGCGGCTCACTGGCTCGATACTGACGCTGAGGGGAAGCAGGGGGAGCAAACAGGATT 723 	724 AGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCTTGT 783 	784 CGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAAC 843 	844 TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGACCATGTGGTTTAATTCGAAGCAAC 903 	904 GCGCAGAACÇTTACCAACCCTTGACATGGCAGGACGCTGGAGAGATTCAGCTTTCTCGT 963 	964 AAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTCGTGTCGTGGAGATGTTCGGT 1023 1111111111111 1111111111111111111	4 TAAGTCCGGCAACGGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAACTCT 108 	1084 ATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGGGATGACGTCAAGTCCTCATGGGCC 1143 	1144 TTACGGGTTGGGCTACACACGTGCTACAATGGTGGTGACAGTGGGTTAATCCCCAAAAGC 1203 	1204 CATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTAATC 1263	1264 GCGGAACAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC 1323
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Nucleotide sequenc Oligonucleotide SE

Bacterium SH134-8

Polynucleotide seg Rhodobacter sphaer Rhodopseudomonas 1

ABL55947 ABL55993

AAH48039

Agrobacterium stel

Bartonella hensela Human blood bacter Nucleotide sequenc Rhodospirillum rDN

AAF90275 ABL54570

Root Stimulating B Sphingomonas pitui

Sphingomonas sp. Sphingomonas 16S

Nucleotide sequenc Rickettsia rickett

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ABL55948 ABL55994 ABL55949 ABL55949 AAZ45682

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New microbes B-396 and A-581-1 - useful for prodn. of all-trans astaxanthin 16S rrna; E-396 (FERM BP-4283); A-581-1 (FERM BP-4671); all-trans astaxanthin; ss: ALIGNMENTS Disclosure; Page 17-18; 20pp; Japanese. DNA derived from 16S ribosomal RNA. AAT15842 standard; DNA; 1452 BP. 94JP-0152078. 94JP-0152078. (NIOC) NIPPON OIL CO LTD. WPI; 1996-110265/12. 04-JUL-1994; 04-JUL-1994; 16-JAN-1996.

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      This sequence represents the 16S rRNA gene from anew species of microbe, B-396 (FERM BP-4283). The microbe is a gram negative pleomorphic rod shaped motile microbe which is aerobic. The GC content of the intracellular DNA is 64-69%. The microbe may be in the production of all-trans astaxanthin in high yield.
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from a culture of the microorganisms designated E-396 (FERM BP-4283) or its mutant A-581-1 (FERN BP-4671). When the protein was fed to white leghorn chickens, the cdlour of their egg yolks improved. The colour improves the colour of foods and drinks.
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pigment-containing foodstuff additive consisting of a microbial culture precipitate with a carotenoid content of at least 3% by weight. The additive is useful in the production of animal foodstuffs with improved resistance to oxygen and light and good long-term storage stability.
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                               the present invention accounts a minimum. The present invention of carotenoid compounds at a specified or varying, ratio by controlling the concentration of oxygen dissolved in the liquid medium during culture. The produced carotenoids are natural pigments, which are use in feed additives, food additives and pharmacenticals. The ratio of carotenoid, compounds obtained can be controlled by varying the concentration of oxygen dissolved in liquid medium during culture. The present sequence represents a specifically claimed 16s ribosomal gene from an unknown organism designated E-396, from the present
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                          present invention describes
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                                                                                                 This DNA sequence encodes a 16S rRNA isolated from a new genus of bacteria, designated E-396. This bacterium is capable of producing carotenoid pigments selected from astaxanthin, adonixanthin, betacarotene, etc. The carotenoid pigments can be produced in industrial quantities and used for feed additives.

(Updated on 25-WAR-2003 to correct PN field.)
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GAUGADAAGUCGGAGGAAGGUGUGGAUGACGUCAAGUCCUCAUGGCCCUUACGGGUUGGG 1139
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                                                                                                                                                                                                                                           This is the nucleotide sequence of the 16S ribosomal RNA gene of Paracoccus marcusii type strain DSM 11574 (also named Paracoccus strain MHI). The 16S rRNA gene can be used to identify this novel Paracoccus species. P. marcusii appeared as a single orange colony contaminating a nutrient agar plate. It produces and secretes carteenoids such as beta-carotene, echimenone, beta-cryptoxanthin, adonizubin, cis-adonizanthin, adonizanthin in vesicles. A process for producing such astranthin and zeaxanthin in vesicles. A process for producing nutrient medium including sources of carbon, nitrogen and inorganic substances, and recovering an individual carotenoid pigment or a mixture of carotenoid pigments from cells, vesicles and/or medium. The carotenoid sare useful as additives for human foods or animal feeds (e.g. in salmonid fish farming) or cosmetics, and provides a ready source of carotenoids that are currently very expensive to synthesise or to extract from natural sources.
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                                                                                                                                                         New Paracoccus marcusil bacterium that produces and secretes carotenoid pigments. - useful, as additives for animal feeds (foods, in cosmetics and as pharmaceuticals
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                                                                                                                                                                                                                      Disclosure; Page 40-41; 55pp; English
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98WO-US14905
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                                                      (FRIË/) FRIEDMAN M M.
(YISS ) YISSUM RES & DEV
                                                                                           Harker M, Hirschberg J;
                                                                                                                               WPI; 1999-153810/13.
                            29-JUL-1997;
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  NO:2.
                                                                                                                                                                                                                                                                                                            The present invention describes a microbial method for producing carotenoid compounds at a specified, or varying, ratio by controlling the concentration of oxygen dissolved in the liquid medum during culture. The produced carotenoids are natural pigments, which are useful in feed additives, food additives and pharmaceuticals. The ratio of the carotenoid compounds obtained can be controlled by varying the concentration of oxygen dissolved in liquid medium during culture. The present sequence represents a 165 ribosomal RNA gene from an unknown organism designated A-581-1 which is given in the exemplification of the
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                     NNA; caroténoid pigment; microbial; carotenoid; pigment; food additive; pharmaceutical; gene; ss.
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Pred. No. 0;
0; Mismatches 11; Indels 3;
16S ribosomal RNA from unknown organism A-581-1 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1426 BP; 349 A; 342 C; 451 G; 284 T; 0 other;
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llarity 99.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
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Matches 1409; Conserv
                      16S ribosomal R
feed_additive;
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                                                                                                                                                                                              Tsubokura A,
                                                       Unidentified
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                                                                                                    10-DEC-2001.
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                                                                                                                                                                                                                                                            The invention relates to a photosynthetic microbe especially sphaeroides FERM P-18033 strain, having azo dye-decomposing amethod can be used for decomposing azo dyes.
                                               Rhodobacter; 16s rRNA; photosynthetic microbe; FERM P-18033;
                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 0;
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                              SEO
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                               rDNA
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.7%;
Matches 1352; Conservative
                             sphaeroides 16s
                                                                                                                                      20-DEC-2000; 2000JP-0387556
                                                                                                                                                          2000JP-0156244
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                                                          azo dye; decomposing; ds
                                                                          Rhodobacter sphaeroides
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GTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGC
           ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT
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                                                                                                                                                                                                    <u> AACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGC</u>
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                                                                                                                                                                                                                                                                         The invention relates to a photosynthetic microbe, preferably handopseudomonas FERM P-17849 strain having azo dye-decomposing activity. The present sequence is that of a Rhodopseudomonas 16S rDNA sequence, useful to the invention
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           P-17849;
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                                                                                                                                                                                                                             compound
           FERM
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Pred. No. 0;
0; Mismatches
         photosynthetic;
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                                                                                                                                                                                                                          for decomposition
                                                                                                                                                                                                                                                   Disclosure; Page 10; 16pp; Japanese.
         S rDNA; photactivity; (
                                                                                                                                                                         (TAIC ) TAIYO KAGAKU KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                85.8%;
                                                                                                                       20-DEC#2000; 2000JP-0387555
                                                                                                                                                26-MAY-2000; 2000JP-0156244
                                                                                                                                                                                                                                                                                                                                                               Query Match 85.8
Best Local Similarity 92.7
Matches 1352; Conservative
         Rhodopseudomonas; 16S
                      azo dye; decomposing
                                                sp.
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                                               Rhodopseudomonas
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              GAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGGAGCAAACAGG
                                                                                                                ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT
                                                                                                                                                                 TCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGG
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                                                                                                                                                                                                                                                  The invention relates to a selenic acid reducing microbe FERM BP-5662 that belongs to Paracoccus genus. It has the ability of reducing 6-valent selenium (8e). Also provided is a method for waste water treatment comprising removing Se from waste water by reducing Se from 6-valent to 4-valent (optionally to an Se simple substance) by microbe (as above) treatment on the active sludge to separate the solid from the liquid. The microbe is useful in water treatment to remove (6-valent) selenium. The microbe is more efficient at removing 6-valent selenium prior art methods. The present sequence represents the nucleotide sequence of 16S rRNA that is used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                         genus
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                         selenic acid reducing microbe, Paracoccus vving selenium in waste water treatment
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1244.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                             Examples; Fig 5, 6; 13pp; Japanese.
                                                                                                                               (MITO ) MITSUBISHI JUKOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%;
93.0%;
                                                                                                              97JP-0136157.
                                                                                     97JP-0136157
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1325; Conservative
                                                                                                                                                                WPI; 1999-073901/07
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
              Paracoccus sp
                                                                                 09-MAY-1997;
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                                                                                                                                                                                                                                                                       The present invention relates to a new beta-hydroxybutyric acid producing microorganism Paracoccus kawaakiensis (FERM P-17644, BP-7059). The new microorganism has properties of paracoccus sp., is unable to grow in a medium containing 0.3% or more of sodium chloride, unable to assimilate potassium nitrate or glutamic acid, but is able to assimilate ammonium sulphate as a nitrogen source. Also, the microorganism has ureasse activity, but is unable to assimilate exylose, mannitol, maltose or lactose. The microorganism is able to assimilate arabinose and sucrose as sole carbon sources. The microorganism is useful for the production of beta hydroxybutyric acid (PHB) and treatment of waste water and reduction of nitrate and removal of nitrogen in waste water. The present sequence
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                                                                                                                                                                                                                 treatment
                                                                                                                                                                                                             new microorganism Paracoccus kawasakiensis is used foiste water and production of beta-hydroxybutyric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1407 BP; 342 A; 341 C; 449 G; 275 T; 0 other;
                                                                                                                                                           SOGO KEN
                                                                                                                             (BIOI-)* BIOINDUSTRY KYOKAI SH.
(AJIN ) AJINOMOTO KK.
(KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU
                                                                                                                                                                                                                                                  Disclosure; Page 4; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                           was used in the present invention.
                                                                               99JP-0330419
                                                                                                       99JP-0330419
  Paracoccus kawasakiensis
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                       JP2001145483-A
                                                                            19-NON-1999;
                                                                                                   19-NOV-1995;
                                                     29-MAY-2001
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245 425 123 AGGAICGGCCCGCGTIGGAITAGGIAGITGGTGGGGGTAATGGCCCACCAAGCCGACGAIC 243 CATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTA 303 365 483 CGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCCGCG 363 AGCAGAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGTAATACGGAGGGGGCTAGC 485 GTIGTICGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAA 543 65 CTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGGAAT AGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGGAGA AGCAGAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGGTAATACGGAGGGGGCTAGC CGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGAAACCCTGATCTAGCCATGCCGCG Gaps DB 22; Length 1407; ις . Score 1227.2; DB 22; Lengt Pred. No. 0; 0; Mismatches 79; Indels 84.5%; 94.0%; Query Match 84.5%; Best Local Similarity 94.0%; Matches 1319; Conservative 124 126 184 186 246 64 244 304 424 184 셤 셤 à 윤 ð à 셤 ò à 8 ö 셤 셤 ö g ö

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               AAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAG
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                                                                                                                                                                                                                                                                                   The invention relates to a novel bacterium, designated SH134-8 in the specification, which is able to decompose the nitrogen-containing sulphur compound HADS (hydroxylaminedisulfonic acid). Bacterium SH134-8 (FERM P-17192) is an aeroble heterotrophic Gram-negative bacterium which is non-motile and has no sugar-assimilating ability. Bacterium SH134-8 as had for decomposing a nitrogen-containing sulphur compound such as HADS in a cost-effective manner e.g., for environmental decontamination. The present sequence represents DNA encoding 16S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                decontamination. The present sequence represents DNA encoding 16S rlbosomal RNA (16S rDNA) from bacterium SH134-8.
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 SH134-8; FERM P-17192; Gram negative; aerobic; heterotrophic; hydroxylaminedisulphonic acid; HADS decomposition; 16S rDNA;
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                                                                                                                                                                                                                                 nitrogen-containing sulfur
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                           Disclosure; Page 4; 5pp; Japanese.
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Local Similarity 92.1%;
Hes 1314; Conservative
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P-17192;
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                                                                JP2000287678-A.
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AAATCCCGGGGCTCAACCCCGGAACTGCCTCCAAAACTCTCAGTCTGGAGTTCGAGAGAG
                                     GAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGGAGCAAACAGG
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illarity 92.1%;
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                                                                                                                                                                           especially
                                                                                                                                                                        The invention relates to a photosynthetic microbe especially sphaeroides FERM P-18033 strain, having azo dye-decomposing method can be used for decomposing azo dyes.
                                                                                                                                                                                                                                                        164; Indels
                                                                                                                                                                                                               Sequence 1484 BP; 353 A; 372 C; 482 G; 277 T; 0 other;
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                                                                                                                                                                                                                                    Score 1113.2;
Pred. No. 0;
0; Mismatches
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                                                                                                                                 New microbe, useful for decomposition
                                                                                                                                                    Example; Page 8; 16pp; Japanese
                                                                                          ROGYO KK
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.1%;
Matches 1288; Conservative
                                                 2000JP-0387556
                                                                    26-MAY-2000; 2000JP-0156244
                                                                                        (TAIC ) TAIYO KAGAKU
                                                                                                          WPI; 2002-288154/33
        JP2002045172-A.
                                                20-DEC-2000;
                             12-FEB-2002
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Pred. No. 0;
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                                                        New microbe, useful 'for decomposition of
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                                                                    Claim 6; Page 8; 16pp; Japanese
                              (TAIC ) TAIYO KAGAKU KOGYO KK
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Best Local Similarity 87.1%;
Matches 1288; Conservative
     20-DEC-2000; 2000JP-0387555
                  26-MAY-2000; 2000JP-0156244
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1206 AGGGTGACCCTTAGCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC 1265 1326 CCGGGCCTTGTACACACCGCCCGTCACACACATGGGAGTTGGCTTTACCTGAAGACGGTGC *TTCTCGTAAGAGGCCTGCACAGGTGCT&CATGGCTGTCGTCAGCTCGTGTGGTGAGA 1146 TCATGGCCCTTACGGGCTGGGCTACACACGTGCTACAATGGCGGTGACAGTGGGACGCGA CCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGTTCTACCCGACGACGNTGC GCTAACCTTCGGGGGGCAGGCGGCCACGGTAGGATCAGCGACTGGGGTGAAGTCGTAACA TAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGA AGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGTTCAGCT-GGAACTCTATGGAAACTGCCGATGATAAGTCG-GAGGAAGGTGTGGGATGACGTCAAGTCC ------GITAATCCCCAAAAGCCATCTCAGTTCGGATTGTCCTGCAACTC GAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGGGGGAATACGTTC 1135 TCATGGGCCTTACGGGTTGGGCTACACGTGCTACAATGGTGGTGACACGTGG-1414 AGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCTCCTT 1452 1446 AGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCTCTT completed: July 28, 2003, 09:25:02 le : 355 secs 1076 1188 1234 1294 1354 786 838 868 957 996 Search con Job time οy qq. Yo g ò g οy g ö 8 셤 ö g õ g O D δ g 2 a ò 185 245 665 237 305 357 365 417 GCCGCGTGAGGTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCGGTGGGGAAGATAATGAC 425 477 537 545 597 605 657 117 125 177 ACGATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGGACTGAGACACGGCCCAGA 297 The invention relates to a photosynthetic microbe, preferably Rhodopseudomonas FERM P-17849 strain having azo dye-decomposing activity. The present sequence is that of a Rhodopseudomonas 16S rDNA sequence, useful to the invention. 65 CTCCTACGGGAGGCAGCAGTGGGGGAATCTTAGACAATGGGGGGCAACCCTGATCTAGCCAT GCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGAC GCTAGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAG GGTACCAGCAGAGAAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGGTAATACGGAGGGG 658 GGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAAC **AGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCAT** AGITIGALCCIGGCICA-GAACGAACGCIGGCGCAGGCTIAACACACAIGCAAGICGAGCG 60 AGACCTTCGGGTCT--AGCGGCGGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTA CGGAATAGCCCCGGGGAAACTGGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTAT GCTAGCGTTGCTCGGAATCACTGGGCGTAAAGCGCACGTAGGCGGCTTTCTAAGTCAGGG GTGAAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGA 598 GAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGT Gaps 1484; 27; Length 718

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1 AGTTTGATCCTGGCTCAGAACGAACGCTGCCGGCAGGCTTAACACACGTGCAAGTCGAGCGA 60
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APPLICANT: Takaki, Mikihiro
APPLICANT: Takaki, Mikihiro
APPLICANT: Takashi
TITLE OF INVENTION: BACTESS FOR PRODUCTION OF CAROTENOIDS USING SAME
NUMBER OF SECUENCES: A
ADDRESSEE: Seed & Berry
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Procompatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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6300 Columbia Center, 701 Fifth Avenue
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US-08-632-470-43
US-08-632-470-32
US-08-632-470-51
US-08-632-470-51
US-08-632-470-40
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches
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NAME: MAKI, David J.
REGISTRATION UNBER: 31,392
REFERENCE/DOCKET NUMBER: 700085,407
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDENESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,943
FILING DATE: 19-UL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08276943
Patent No. 5607839
GENERAL INFORMATION:
- APPLICANT: TSubokura, Akira
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                                              STREET:
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5773.769 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             - nucleic search, using sw model
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us-10-049-228-1.rni

Db	Db	RESULT 2 US-08-716-841-1 Sequence 1, Application US/08716841 Patent No. 3858761 GENERAL INFORMATION: APPLICANT: Tsubokura, Akira APPLICANT: Tsubokura, Hisashi APPLICANT: Takaki, Mikihiro	Kiyota, WENTION: WENTION: BEQUENCES: NCE ADDRE Seed 6		SOUTHARK: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/276,943 FILING DATE: 19-JUL-1994	NAME: Mak1, David J NAME: Mak1, David J REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 700085.407 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-490 TELEFAX: 3723836 SEEDAMBERY INFORMATION FOR SEQ ID NO: 1:	SEQUENCE CHARATERIZOTICS: LENGTH: 1452 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to FRNA
		0 0 0 0	0000	0 0 0 0		0 0 0 0	
		ACCAGCAGAAGAAGCCCCGGGCTAACTCCGTGCCAGCGGCGGTAATACGGAGGGGGGCT	541 AANTCCCAGGGCTCAACCTTGGAACTGCAACTATCAGTGTCTGGAGTTCGAGAGAG 600 [661 GAAGGCGCCTCACTGGCTCGACGCTGAGGTGCGAAAGCGTGGGGGAGCAACAGG 720 [111111111111111111111111111111111111	781 TGTCGGTGTCACCTAACGGATTAACCATTCCGCCTGGGAGTACGGTCGCAAGATTAA 840		1021 GGTTAAGTCCGGCAACGCAACCCACGTCTAGTTGCAGCAATTCAGTTGGAACC 1080 1021 GGTTAAGTCCGGCAACGCGCAACCGCAGCAGCAGCAGCAGCAAGTTGGGAACC 1080 1081 TCTATGGAACTGCGGATGATAAGTCGGAGGAAGTGGGAATGAGTGGGAAC 1080 11081 TCTATGGAACTGCGGATGATAAGTCGGAGGAAGTGTGGGAATGACGTCAAGTCCTCATGG 1140
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STREET: 2940 Birchtree lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of Am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Friedmam, Mark M. REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Patent No. 5935808
GENERAL INFORMATION:
APPLICANT: JOSEPH HIRSCHDERG. and Mark Harker
TITLE OF INVENTION: NOVEL CAROTENOID-PRODUCING BACTERIAL
TITLE OF INVENTION: SPECIES AND PROCESS FOR PRODUCTION
TITLE OF INVENTION: OF CAROTENOIDS USINGSAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: t converted Sheinbein microdisk MEDIOM TYPE: 1.44 megabyte, 3.5" microdis)
COMPUTER: Twinhead* Slimnote-890TX
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 cor
SOFTWARE: an ASCII file
CUSTRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,518A Robert

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Fred. No. 0;
0; Mismatches
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APPLICANT: MANOME, AKITA
APPLICANT: WURANE, RYUICHIO
TITLE OF INVENTION: METHOD FOR
FILE REFERENCE: 0010-1089-0X
CURRENT APPLICATION NUMBER: US/09/517,744B
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09517744B Patent No. 6391576 GENERAL INFORMATION:
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Best Local Similarity 94.0%;
Matches 1319; Conservative (
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SEQ ID NO 1
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US-09-517-744B-1
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Best Local Similarity 80.0%; Pred. No. 0;
Matches 1145; Conservative 282; Mismatches
                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430
972-3-5625554
                                                 TYPE: nucleic acid
STRANDEDNESS: double
TÖPOLOGY: linear
US-08-902-518A-1
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APPLICANT: DISPIRITO, ALAN A.
APPLICANT: DO. YOUNG S.
APPLICANT: DO. YOUNG S.
APPLICANT: DO. YOUNG S.
APPLICANT: DO. YOUNG S.
APPLICANT: PHILLIPS, GREGORY J.
APPLICANT: ALH, JAMES A.
TITLE OF INVENTION: LITESTOCK WASTE LAGOONS AND BIOMASS PRODUCTION
FILE OF INVENTION: LITESTOCK WASTE LAGOONS AND BIOMASS PRODUCTION
FILE OF INVENTION NUMBER: US/09/565,063
CURRENT APPLICATION NUMBER: US/09/565,063
FRIOR APPLICATION NUMBER: 60/133,087
PRIOR APPLICATION NUMBER: 60/133,087
PRIOR APPLICATION OF SEQ ID NOS: 6
SOFTWARE: PALENTING DATE: 1999-05-07
SOFTWARE: PALENTING DATE: 1999-05-07
SOFTWARE: PALENTING DATE: LAGOONS AND BIOMASS PRODUCTION
SEQ ID NO 2
LENGTH: 1419
                                 CCATGGGAGTTGGTTCTACCCGACGACGNTGCGGTAACCTTC--GGGGGGCAGGCGGCA 1379
                                         CCATGGGAATTGGGTCTACCCGACGACGGTGCGCTAACCCGCAAGGGAGGCAGCCGGCCA 1384
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Pred. No. 0;
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                                                                                                                       US-09-565-063-2; Sequence 2, Application US/09565063; Patent No. 6489156; GENERAL INFORMATION:
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ORGANISM: Rhodobacter
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; APPLICANT: Lindner, Luthe

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1383 1323 1263 1203 1143 1023 ë 139 199 499 619 619 739 259 319 379 439 559 903 843 783 799 723 GGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGG 859 963 79 560 TGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGTGGAATTCCGAGTG CAGAATGGCCTTCGATACTGGGACGCTWGAGTATGGTAGAGGTTGGTGGAACTGCGAATG CACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCTTGTCGGTGTCACACCTAAC CACGCCGTAAACGATGAATGCCAGCTGTTGGGGTGCTTGCACCAGTAGCGCAGCTAAC GGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGGAATAGCCCCGGGAAACTGG 140 GAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAGGATCGGCCCGCGTT GGATTAGGTAGTTGGGGGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTTGAGA TAGGGTTGTAAAGCTCTTTCAGGTGGGAAGATAATGACGGTACCAGCAGAAGAGCCCCG GCTAACTCCGTGCCAGCAGCGGGGTAATACGGAGGGGGCTAGCGTTGTTCGGAATTACT GGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAATCCCAGGGCTCAACCT new human blood bacterium 20 ACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGGGGAGACCTTCGGGTCTAGCGGC Gaps 23; Length 1502; Indels DB 3; Ouery Match 74.8%; Score 1086.4; DB 3; Best Local Similarity 86.2%; Pred. No. 0; Matches 1245; Conservative 0; Mismatches 177; Ø APPLICANT: Macphee, Kathleen
TITLE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026
CURRENT APPLICATION NUMBER: US/09/187,946
CURRENT FILING DATE: 1998-11-02
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 20
SEQ ID NOS: 20
LENGTH: 1502) OTHER INFORMATION: 58 16S FRNA sequence of US-09-187-946-2 ORGANISM: unknown 1382. 200 380 440 200 80 962 620 902 740 782 800 TYPE: DNA FEATURE: 윱 ö 셤 ô

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                                                                                                                                                                                                                                                     Score 1036.4; I Pred. No. 0; 0; Mismatches
             CLASSIFICATION: 435
ATORNEY-AGENT INFORMATION:
NAME: BERIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
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                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic) US-08-632-470-52
                                                                                                           TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 52.
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                       71.4%;
86.8%;
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Best Local Similarity
Matches 1230; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE FRAGMENTS CAPABLE OF
HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA
THEIR USE AS PROBES OR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
                                                                                                                                                                                                                                                                                                                         CACACGTGCTACAATGGTGGTGACAGTGG------
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F: P.O. BOX 19928
ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MABLIAT, CLAUDE
APPLICANT: RADULTA, DIDLER
TITLE OF INVENTION: NUCLEOT
TITLE OF INVENTION: THERE UI
TITLE OF INVENTION: THERE UI
NUMBER OF SEQUENCES: 53
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US-08-632-470-52
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                                                                                                                                                                                                                                                                                                                                                                 Score 987.4; D. Pred. No. 0; Mismatches
        FILING DATE: 22-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 1826/47986
TELECOMMUNICATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                   68.0%;
ilarity 83.7%;
Conservative (
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: TRNA
US-08-995-960-1
NUMBER
                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 1210; Conserv
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                                                                              852 ATTGACGGGGGCCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAA
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Patent No. 6030818

GENERAL INFORMATION

APPLICANT: PAGI, Michel

APPLICANT: BOISSINOT, Mautice

APPLICANT: HILLE, Marie-Claude

APPLICANT: HARDEY, Marie-Claude

APPLICANT: HARVEY, Marie-Claude

APPLICANT: HARVEY, Marie-Claude

TITLE OF INVENTION: BACTERIAL MASS PRODUCTION

TITLE OF INVENTION: OF TAXANES AND PACLITAXEL

NUMBER OF SEQUENCES: 18
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: Window
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ADDRESSEE: Dike, Bro
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US-08-995-960-1
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Gaps

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Length 1556;

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Score 980.2; I
Pred. No. 0;
0; Mismatches
                                                                                    FILING DATE: 08-001-1996
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                             67.5%;
llarity 81.8%;
Conservative
                                                                                                                                                                                            TELEFAX: (703)-836-2787.
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      1508 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCTTCGGGTCTAGC
                                                                                                                                                                                                                                                  TYPE: nucleic acid_
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 1220; Conserv
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                                                                             837
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                                        892 GTCTTTGGGTGGCGCAGCTAACGCATTAAGTTATCCGCCTGGGGAGTACGGCGGCAAGGT
                                                                                                                                               1431 CAGGCCTTGTACACACCCCCGTCACACGAGGGGGGTTGACCCGAAGGCGTTGCG
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                                                                            779 CT-TGTCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGAT
                                                                                                                                TAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGA
                                                                                                                                                                                  AGCAACGCGCAGAACCTTACCAACCCTTGACATGCCAGGACCGCT - - GGAGAGATTCAGC
                                                                                                                                                                                                                                                                                       TGTTCGGTTAAGTCCGGCAACGAGCGCAACCACGTCCCTAGTTGCCAGCAATTCAGTTG
                                                                                                                                                                                                                                                                                                                                            GGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCT
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Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABLICAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: WUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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US-08-632-470-44
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLING DATE: US/08/632,470
FILING DATE: 08-JUL-1996
                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                   Organism:strain
                                                                                                                                                                Length
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                                                                                                                                                                                  225;
                                                                                                                                                                 DB 4;
                                                                                                                                                             67.1%; Score 973.6;
82.4%; Pred. No. 0;
ive 0; Mismatches
EARLIER APPLICATION NUMBER: JP 10-193472
EARLIER FILING DATE: 1998-07-08
EARLIER APPLICATION NUMBER: JP 10-310398
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 2
                                                                                                                               OTHER INFORMATION: Description of Unknown
                                                                                                                                                                         Best Local Similarity 82.4 Matches 1186; Conservative
                                                                                                      TYPE: DNA ORGANISM: Unknown
                                                                                           LENGTH: 1436
                                                                                                                                    ; OTHER INFORM
US-09-347-001-2
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Fatent No. 633517
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasushiro
APPLICANT: TAKEUCHI. Sonoko
APPLICANT: TONOUCHI. Naoto
APPLICANT: UNUMENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
TITLE REFERENCE: US/09/347,001A
CURRENT APPLICATION NUMBER: US/09/347,001A
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                                                                                                                               TGATCCTGGCTCAGAACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGGGCAGACC
 Unknown Organism:strain
                                                                     Score 960.4; DB 4;
Pred. No. 6.1e-315;
0; Mismatches 228;
                   ; OTHER INFORMATION: N at position 1365 is A, T, G, US-09-347-001-1
Description of
                                                                     Query Match 66.1%;
Best Local Similarity 82.3%;
Matches 1183; Conservative
OTHER INFORMATION:
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APPLICANT: TAKEUCHI, Sonoko

APPLICANT: TAKEUCHI, Sonoko

APPLICANT: TOJOIMA, Yasusko

APPLICANT: TONOUCHI, Naoto

APPLICANT: TONOUCHI, Naoto

APPLICANT: TONOUCHI, Ryosuke

APPLICANT: TOKOZEKÍ, Kenzo

TITLE OF INVENTION: D-XXLULOSE

FILE REFERENCE: 0010-1015-0

CURRENT APPLICATION: NUMBER: US/09/347,001A

CURRENT FILING DATE: 1998-07-02

EARLIER APPLICATION NUMBER: JP 10-193472

EARLIER FILING DATE: 1998-07-08

EARLIER FILING DATE: 1998-10-30

EARLIER FILING DATE: 1999-11-2044
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                                                                                                 ACCCCCAGAACCTTACCAACCCTTGACATGCCAGGACCCCTGGAGAGTTCAGCTTTCTC
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ORGANISM: Unknown Organism
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                                        Score 944.2; DB 2;
Pred. No. 2e-309;
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                                        65.0%;
llarity 80.2%;
Conservative
                                           Query Match
Best Local Similarity
Matches 1199; Conserv
MOLECULE TYPE:
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US-08-632-470-49
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APPLICANT: RAGULT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA )
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/08632470 Patent No. 5976791
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P.O. BOX 19928
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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TOPOLOGY: linear
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MEDIUM TYPE: Floppy
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CITY: ALEXI
STATE: VA
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 81.7%;
Matches 1179; Conservative
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APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMËRS
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960 CTTCTTAACAGAAGGGCGCAGTTCGGCTGGGCCTCGCACAGGTGCTGCATGGCTGTGTCTC 1019
                              1000 AGCTCGTGTCGTGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTT
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                                                                                            1060.GCCAGCAATTCA-GTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAGGTGT
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                                               1020 AGCTCGTGTGTGTGTGTGTGTGTTAGTTCCCGCAACGAGCGCAACCCTCATAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-UUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
21P: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08632470 Patent No. 5976791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WP
IELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & B
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Score 944; DB 2; 1
Pred. No. 2.3e-309;
0; Mismatches 221;
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TYPE: nucleic acid
STRANDEDNESS: single
LENGTH: 1440 base
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                                                TGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTC
                                                           AACTCGAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGGCGGTGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABLIAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR 1
TITLE OF LOUGH SPECIFICATION OR 19928
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
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NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEPHONE: (703)-836-5400
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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USA
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US-08-632-470-36
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                                                                                                                                                                     CTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATT
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                                                                                                                                                                                                                          GGTCTAGC-------GCCGGACGACGGTGAGTAACGCGTGGGAACGTGCCCTTCT
                                                                                                                                              43;
                                                                 Length 1440;
                                                          Score 944; DB 2; 1
Pred, No. 2.3e-309;
0; Mismatches 221;
; MOLECULE TYPE: DNA (genomic)
US-08-632-470-36
                                                              Query Match 65.0%;
Best Local Similarity 81.7%;
Matches 1179; Conservative
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                                                                                                                                                                                                                      CTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATT
                                                                                                                                                                                                                                                                                                                                                                                               TATCGGAGAAGGATCGGCCCCCCCTTGGATTAGGTAGTTGGTGGGGGTAATGGCCCACCAAG
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                                                                                                                                                                         Gaps
                                                                                                                                          Length
                                                                                                                                        Score 942.4; DB 2;
Pred. No. 8.1e-309;
0; Mismatches 222;
              SEQUENCE CHARACTERISTICS:

LENGTH: 1440 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-632-470-35
                                                                                                                                        64.9%;
larity 81.6%;
Conservative
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Best Local Similarity
Matches 1178; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 CGATGTTACGCGAAAAACTTTACCAACCCTTGACATGGTGGTCGTGAATCGCAGAGATGC
                             TCAGCTTTCTCGTAAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTCGTCTCGTGTCG
                                             TGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTC
                                                                                                                                                       A-GTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCA
                                                                                                                                                                                                                   AGTCCTCATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGGTGGTGACAGTGG--
                                                                                                                                                                                                                                                                                  ------GTTAATCCCCAAAAGCCATCTCAGTTCGGATTGTCTCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MADILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLECTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: THEIR USE'AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET UMBER: WPB 38238
TELECOMMUNICATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OLIFF & BERIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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US-08-632-470-35
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180 234 240 294

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AT 950 GC 959	CG 1010 	TC 1070 TA 1079	CA 1129 CA 1139	1187 GA 1199	GC 1228 	TA 1288 TA 1319	AC 1348 GT 1379	CG 1408 		
CTGGAGAG GATCGCAGAGAT	GTCAGCTCGTGT 	GTTGCCAGCAAT TTTGCCAGCGG	itgiggaigacgi tgggacgacgi	TGGTGACAGTGG TGTTTACAGAGG	GGATTGTCCTC1 	TGCCGCGGTGA TGCCGCGGTGA	TTCTACCGACC	ACTGGGGTGAAG1 		
CGAAGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGAT 	TCAGCTTTCTCGTAAGAGCCGGCACACAGGTGCTGCATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT	E AGABTGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTC 11 1 1 1 1 1 1 1 1	a-gttgggaactctatggaaactgccgatgataagtcggaggaaggtgtggatgacgtc 	AGTCCTCATGGGCCTTACGGGTTGGGCTACACAGTGCTACAATGGTGGACAGTGG	1188GTTAATCCCCAAAAGCCATCTCAGTTCGGATTGTCCTCTGC	aactcgagggcatgaagtggaatcgctagtaatcgcggaacagcatgccggggaata 	CGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGTTCTACCCGACGAC	GNTGCGCTAACCTTCGGGGGGCAGGCGGCCACGGTAGGATCAGCGACTGGGGTGAAGTCG 		
CCAACCCTTGAC	GCACACAGGTGC 	CAACGAGCGCAJ 	TGCCGATGATA 	TGGGCTACACAC 	PATCCCAAAA AATCCTAAAA	ATCGCTAGTAA: 	CGCCCGTCACA(AGGCGGCCACG		
GCAGAACCITA GAAAACCITA	CGTAAGAGACCT 	GTTAAGTCCGG	CTCTATGGAAAC CTATAAGAAAAC	SGCCTTACGGGT 	CGACGTGGAGCA	CATGAAGTTGGA 	CCTTGTACACAC 	CCTTCGGGGGGG 		
					AGCAAGACGG	AACTCGAGGGG		GNTGCGCTAAK GGTAAGCTAAK	TAA 1411 AA 1440	
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Search completed: July 28, 2003, 11:43:55 Job time: 118 secs

Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 158, App Sequence 158, App Sequence 2, Appli Sequence 2, Appli Sequence 24, Appli Sequence 24, Appli Sequence 4, Appli Sequence 6, Appli

0 US-09-951-720-1 1 US-09-791-610-1 4 US-10-266-787-5 4 US-10-266-787-5 4 US-10-105-518-5 4 US-10-105-518-5 4 US-10-105-905-1 6 US-09-967-376-1 7 US-09-727-297-4 US-09-727-297-4 US-09-727-297-4 US-09-727-74-3 US-09-911-1938-158 US-09-912-020-82 US-09-912-020-82

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Sequence 3, Appli Sequence 12, Appl Sequence 12, Appl Sequence 19, Appl

Sequence 1, Appl Sequence 1, Appl

US-09-974-300-8479

US-09-027

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57.2 1549
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57.2 1549
56.4 1544
56.2 1553
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56.0 1830121
55.0 1830121
55.7 1424
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8414.261 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_NBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USOB_NBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
                                                                                                                                                    . July 28, 2003, 10:53:33 ; Search time 356 Seconds
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                    1439767 segs, 1031500376 residues
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Maximum Match 100%
Listing first 45 summaries
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    nucleic search, using sw model

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1452
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Perfect score:
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TYPE: DNA

ORGANISM: Unknown

FEBATURE:
OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA or OTHER INFORMATION: 96 strain
NAME/KEY: misc_feature

LOCATION: (1350). (1350)

OTHER INFORMATION: 1 is A, C, G or T

US-10-049-228-1 ö 61 GACCTTCGGGTCTAGCGGGGGGGGGGGGGGGGGACGTGCCTTCTACGG 120 1 AGTITGATCCTGGCTCAGAACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGA 60 1 AGTTTGATCCTGGCTCAGAACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAAGGCGA 60 Gaps ; 0 Sequence 1, Application US/10049228
Publication No. US20030044886A1
Sequence 1, INFORMATION:
APPLICANT: TSUBOKURA, Akira
APPLICANT: MIZUTA, HATUYOSh1
TILE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
FILE REFERENCE: 3833-10003
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: PCT/JP01/04874
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 2
SCOTUMBER: Patentin version 3:1
SEQ ID NO 1
LENGTH: 1452 Query Match
99.9%; Score 1451; DB 14; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Indels g à

Sequence 1, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 1, Appl1

US-09-894-467-1 US-09-847-513A-1 US-10-007-725-6 US-10-007-725-5

US-09-791-592-1 US-09-745-476-1 US-09-821-016-5 US-09-748-205-1 US-09-793-920A-1

US-09-726-774-12 US-09-894-467-2 US-09-900-876-2 US-09-902-693-2 US-09-902-693-1

1380 1093.6 1086.4 1044.6 973.6 960.4

1490 1436 1438 1208 105184

Description

Query '

Score

Result No.

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Oy 1201 AGCCATCTCAGATTGTCCTCTGCAACTCGAGGCATGAAGTTGGAATCGCTAGTA .1260	1201 AGCCATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGCAAGTA		Oy 1321 ACCATGGGAGTTGGTTCTACCCGACGACGACGCTAACCTTCGGGGGGCGGCGCCAC 1380	Qy 1381 GGTAGGACTGGGGTGAAGTCGTAACAAGGTAGGGGAACCTGCGGCTG 1440	Oy 1441 GATCACTCTT 1452 Db 1441 GATCACTCTT 1452	RESULT 2 US-10-049-228-2 ; Sequence 2, Application US/10049228		; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS; FILE REFERENCE: 3831-0003; CURRENT APPLICATION NUMBER: 105/10/049,228; CURRENT FILING DATE: 2002-02-11	PRIOR PAPLICATION NUMBER: PCT/JP01/04874 PRIOR FILING DATE: 2001-06-06 PRIOR APPLICATION NUMBER: JP 2000-175124 PRIOR FILING DATE: 2000-06-12	; NUMBER OF SEQ ID NOS: 2 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 2 ; LENGTH: 1426	TYPE: DNA ORGANISM: Unknown FEATURE: OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA	INFORMATION: 81-1 strai 228-2 tch 95.0%;	Best Local Similarity 99.0%; Pred. No. 0; Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2; Oy 1 AGTTGATCCTGGCTCAGAACGAACGCTGGCGGCAGCTTAACACATGCAAGTGGAGCG 60	Db 4 AGTTGATCCTGGCTCAGAACGCTGGCGGCAGCCTTAACACATGCAAGTCGAGCGA 63 Oy 61 GACCTTCGGGTCTAGGGGGGACGGGGGAGTAAACGCTGGGAAGTCTTAGGG 120	Db 64 GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTACGG 123 Qy 121 AATAGCCCGGGAAACTGGGGAGTAATACGCCTTTGGGGGAAAGATTATGG 180		14111111111111111111111111111111111111	244 ATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACCGGCCCAGACTC 301 CTACGGGAGGAGGAGGGAATCTTAGACAATGGGGGCCAACCTGATCTAGGCGCCAACCTGATCTAGGCGGCCAACCTGATCTAGGCGGCCAACCTGATCTAGGCGGCCAACCTGATCTAGGCCAACCTGATCTAGCCATGCC
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Db 1383 ACGGTAGGATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCC 1425	RESULT 3 US-09-726-774-12 ; Sequence 12, Application US/09726774	<pre>; Patent No. US20020082226A1 ; GENERAL INFORMATION: ; APPLICANT: Iversen, Patrick L. ; TITLE OF INVENTION: Antisense Antibacterial Method and</pre>		FRIOR APPLICATION NUMBER: US 60/168,150 ; FRIOR ELING DATE: 1999-11-29 ; NUMBER OF SEQ ID NOS: 139 ; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ ID NO 12 ; LENGTH: 1466 ; TYPE: DNA ; ORGANISM: Bartonella henselae		.3%; Score 1093.6; DB 9; Length 1466;	Matches 12/8; Conservative U; Mismatches 151; Indels 29; Gaps 8 TCCTGGCTCAGAACGAACGCTGGCGCAGGCTTAACACACATGCAAGCG-AGACCTT	1 TCCTGGCTCAGGATGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGCACTCATT 67 CGGGTCTAGCGGACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGGAATAGC 1	61 TAGAGTGAGCGGCAGACGGGTGAGTAACGCGTGGGAATCTACCCTTTTCTACGGAATAAC 127 CCCGGGAAACTGGGAGTAATAACGCTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAGG 	121 ACAGAGAAATTTGTGCTAATACCGTATACGTCCTACTGGAGAAAGATTTATCGGAGAAGG 187 ATCGGCCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCGACGACGATCAT 11	181 AIGAGCCCGCGTTGGATTAGCTAGTTGGTGAGGTAAAGGCTGACCAAGGCGACGATCCAT 247 AGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGAGACAGGCCCAGACTCTACGG [241 AGCTGGTCTGAGAGGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGG 307 GAGGCAGCAGCAGTGGGGAATCTTAGACAATGGGGGGCAACCCTGATCTAGCGATGCGGTGA	301 GAGGCAGCAGCAGTGGGGAATATTGGACAATGGGGGGCAACCCTGATCCAGCCATGCCGGTGA 367 GTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGTACCAGC	361 GIGAIGAAGGCCCIAGGGITGIAAAGCICTITCACGGGTGAAGAIAATGACGGTAACCGG 427 AGAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCAGGGGTAATACGGAGGGGGGTAGCGTT	421 AGAAGAAGCCCGGGTAACTTCGTGCCAGCAGCGGGTAATACGAAGGGGGGTAGTTT 487 GTTCGGAATTACTGGGGGTAAAGCGCACGTAGGCGGAACTGGAAAGTCAGAAGTGAAATCC	481 GITCGGAITTACIGGGCGRAAAGCGCAIGTAGGCGGGATAITTAAGTCAGAGGTCAAATCC 547 CAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGGGGT (DD 541 CAGGGTCAACCCTGGAACTGCCTTTGATACTGGATATCTTGAGTATGGAAGAGTGAGT
	CTTAGGGTTGTAAAGCTC [†] TTCAGCTGGGAAGATAAT 		agcgcacgtaggcggactggaaagtca 	OY 541 AAATCCCAGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGG 600	OY 601 GTGAGTGGAATTCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACCAGTGGC 660 	OY 661 GAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGG 720 DD 111111111111111111111111111111111111	OY 721 ATTAGATACCTGGTAGTCCACGCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT 780	OY 781 TGTCGGTGTCACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAA 840	QY B41 AACTCAAAGGAATTGACGGGGCCCCCCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGC 900 L	OY 901 AACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACGCTGGAGAGATTCAGCTTTCT 960	QY 961 CGTAAGAGACTGCACACAGAGTGCTGCATGGCTGTCGTGGTGGTTC 1020 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1021 GGTTAAGTCCGGCAACGAGCGCAACCGCTCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080	OY 1081 TCTATGGAAACTGCCGATGATAAGTCGGAGGAGGAGGGTGGGCGTCAAGTCCTCATGG 1140	OY 1141 GCCTTACGGGTTGGCTACACGTGCTACAATGGTGGTGACAGTGGGTTAATCCCCAAA 1200 	OY 1201 AGCCATCTCAGTTGGGATTGTCCTCTGGAACTCGAGGGCATGAGTTGGAATCGCTAGTA 1260	OY 1261 ATCGCGGAACAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACGCCCGTCAC 1320	QY 1321 ACCATGGGAGTTGGTTCTACCGACGACGACGACGCTAACCTTCGGGGGGGCAGGCGGCC 1378 Db 1323 ACCATGGGAGTTGGTTCTACCCGACGACGACGCTGGGCTAACCCTTCGGGGAGGCAGGC	OY 1379 ACGGTAGGATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCC 1421

20 NOS:

A SEO TYPE: DNA ORGANISM: Unknown

FEATURE:

LENGTH: 1502

SEQ ID NO 2 Q.

NUMBER

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CGCCTGGATCGGAGACAGGTGCTGCATGGCTGTCGTCAGCTCTGTGGG 1020
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APPLICANT: MacPhee, Kathleen
TITLE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026b
CURRENT APPLICATION NUMBER: US/09/894,467
CURRENT APPLICATION NUMBER: US 09/187,946
PRIOR FILING DATE: 1998-11-02
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 58 rRNA sequence of a new human blood bacterium
                                 Length 1502;
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                              Score 1086.4; DB 10;
Pred. No. 1.7e-285;
0; Mismatches 177; 1
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COTHER INFORMATION:
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Best Local Similarity 83.9%;
Matches 1241; Conservative
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                                                                                                                                                                                                                                                                              LOCATION: (988)...(988)
OTHER INFORMATION: n = c, g.
NAME/KEY: misc_feature
LOCATION: (1045)...(1045)
OTHER INFORMATION: n = c, g
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LOCATION: (1332)..(1333)
OTHER INFORMATION: n = c, g
NAME/KEY: misc_feature
LOCATION: (1408)..(1408)
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INFORMATION: n = C,
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                                LOCATION: (490)...(490)
OTHER INFORMATION: n = c
NAME/KEY: MISC_feature
LOCATION: (596)...(596)
OTHER INFORMATION: n = c
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LOCATION: (910)..(911)
OTHER INFORMATION: n =
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LOCATION: (1437)...(1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09900876
Patent No. US20020045990A1
GENERAL INFORMATION:
PAPLICANT: WATANNE, KATSUJI
APPLICANT: WATANNE, MITSURU
TITLE OF INVENTION: MTHOD AND SYSTEM FOR SEARCHING FOR RELATIONSHIPS BETWEEN BASE STILE REFERENCE: 210847USOX
CURRENT APPLICATION NUMBER: US/09/900,876
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                             .040 ČĠĊAACCCACGTCCCTAGTTGCCAGCAATTCAGTTGGGAACTCTATGGAAACTGCCGATG 1099
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                                                                                                                         ACCCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCTCGTAAGAGACCTGCACACA
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ORGANISM: Rhodospirillum salexigens
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1490
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OTHER INFORMATION: n = c,
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OTHER INFORMATION: n = c,
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OTHER INFORMATION: n = c,
NAME/KEY: misc_feature
LOCATION: (485)..(485)
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op qa		; APPLICANT: MIHARA, Yasushiro ; APPLICANT: TAKEUCHI, Sonoko ; APPLICANT: JOITMA, YASUKO
oy Ob	539 TGAAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGGG 598 1	APPLICANT: TONOUCH, Nactory APPLICANT: FUDOU, Ryosuke APPLICANT: YOKOZEKI, Kenzo
Oy Db	\$99 AGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTG 658 	TITE OF INVENTION: NOVEL NICKE ; FILE REFERENCE: 0010-1015-0 ; CURRENT APPLICATION NUMBER: US
Oy Db	659 GCGRAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGAAGCGTGGGGAAGCAAACA 718 	CURRENT FILING DATE: 2001-07-07-08-08-08-08-08-08-08-08-08-08-08-08-08-
Oy Db	719 GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCAT- 777 	; PRIOR FILING DATE: 1998-0/-08 ; PRIOR FILING DATE: 1998-10-30 ; PRIOR FILING DATE: 1998-10-30 ; PRIOR APPLICATION NUMBER: JP 1
Oy Ob	778 GCTTGTCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGAT 837	; PRIOR FILING DATE: 1999-01-20; NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 2
Oy Db	838 TAAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGA 897 	; TYPE: DNA ; TYPE: DNA ; ORGANISM: Unknown Organism ; FEATURE:
Qy Dp	898 AGCAACGCGCAGAACCTTACCAACCCTTGACAFGGCAGGACGCTGGAGAGATTCAGC 955 	GOTHER INFORMATION: Descripti US-09-902-693-2 Query Match 67.18;
oy O	956 TTTCTCGTAAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTCGTGTGCTGTGAAGAAGACTGCTGAGA 1015 	Best Local Similarity 82.4%; Matches 1186; Conservative Oy 5 TGATCCTGGCTCAGAACGA
oy Dp	1016 TGTTCGGTTAAGTCCGGCAACGGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTG 1075 1029 TGTTGGGTTAAGTCCCNCAACGAGCGCAACCCTCGCCCTTAGTTGCCAGC-ATTGGTTG 1087	Db 1 TGATCCTGGCTCAGAGCG, Oy 65 TTGGGGTCTAGCGGAG
S G	1076 GGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGA	Db 61 TTCGGGTTAGTGGCGGAC Qy 125 GCCCGGGAAACTGGGAG
ÇŅ Dp	CCTTACGGGTTGGGCTACACACGTGCTACAATGGTGGTGACA	Db 121 ACACCGGGAAACTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC
λö	GIGGGTIAATCCCCAAAAGCCATCTCAGITCGGATTGTCCTGCAACTCG	181
o de	1208 CCTGCGAGGGTGAGCGAATCTCTAAAAGCCGTCTCAGTTCGGGATTGTTCTGCAACTCG 1267 1235 AGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGGGGTGAATACGTTCC 1294	Oy 243 CCATAGCIGGITIGAGAGG
QQ	1268 AGAGCAFGAAGGFGGAAFCGCTAGTAAFCGCGGATCAGCAFGCCGGGGGAATACGTTCC 1327	· Qy 303 ACGGAGGCAGTGGG
දු දු	1295 CGGGCCTTGTACACACCGCCCGTCACCACCATGGGAGTTGGTTCTACCCGACGATGCG 1354	Db 301 ACGGGAGCCAGCAGGGGGGGGGGGGGGGGGGGGGGGGG
οy	1355 CTAACC - TTGGGGGGGCGGGCGCGACGGTAGGATCAGCGACTGGGGTGAAGTGTACTAC 1412	Db 361 GTGTGAAGAAGCTCTT
a &	GAAAGGGGGCAGNCGGCCAC GCGTAGGGGAACCTGCGGCTG	Oy 423 CAGCAGAAGAAGCCCCGGG
QQ		Qy 483 CGTTGTTCGGAATTACTGC
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RESULT 6 US-09-902-693-2

ACGGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGGAATA 124 GTAATACCGTATACGCCCTTTGGGGGAAAG -- ATTTATCGGAG 182 CROORGANISM AND METHOD FOR PRODUCING XYLITOL OR OSE SGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACGAT 242 GGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCT 302 ATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGT 602 64 9 Gaps 28; Length 1436; ion of Unknown Organism:strain S877 Indels Score 973.6; DB 9; Pred. No. 7.8e-255; 0; Mismatches 225; US/09/902,693 7-12 10-310398 0 10-193472 11-12244 /347,001 902693 q ò

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APPLICANT: TAKEUCHI, Sonoko
APPLICANT: JOJIMA, Yasuko
APPLICANT: TONOUCHI, Naoto
APPLICANT: FUDOU, Ryosuke
APPLICANT: YOKOZEKI, Kenzo
APPLICANT: TONOUCHI, NAOTO
APPLICANT: TONOUCHI, NAOTO
APPLICANT: TONOUCHI, NAOTO
APPLICANT: FUDOU, RYOSUKE
APPLICANT: PUDOU, RYOSUKE
APPLICANT: PUDOU, RYOSUKE
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GAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGA
                                                          AGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGAT
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Patent No. US20020061561A1
GENERAL INFORMATION:
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US-09-902-693-1
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OTHER INFORMATION: Description of Unknown Organism:strain
OTHER INFORMATION: N at position 1365 is A, T, G, or C
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; Pred. No. 3e-251;
. 0; Mismatches 228;
CURRENT APPLICATION NUMBER: US/09/902,693 CURRENT FILING DATE: 2001-07-12
                               PRIOR APPLICATION NUMBER: 09/347, 001
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 09/347, 001
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1999-10-20
NUMBER: 0F FLING DATE: 1999-01-20
NUMBER: PAtentin Ver. 2.1
                                                                         10-193472
                                                                                                              10-310398
                                                                                                                                                 11-12244
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Best Local Similarity 82.3%;
Matches 1183; Conservative
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                    TAGATACCCTGGTAGTCCACGCTGTAAACGATGTGTGCTGGATGTTGGGTAACTTAGTTA
                                       -TCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGGAGTACGGTCGCAAGATTAAA
                                                   CTCAGTGTCGAAGCTAACGCGCTAAGCACCGCCTGGGAAGTACGGCCGCAAGGTTGAA
                                                                                                                           ACGCGCAGAACCTTACCAACCCTTGACAT-GGCAGGACCGCTGGAGAGTTCAGCTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown
PETATURE:
NAME/KEY: gene
LOCATION: nt40; nt60
OTHER INFORMATION: Entire Rb 165 rRNA gene sequence of a new human
OTHER INFORMATION: blood bacterium (HBB). The identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09894467
Patent No. US20020155519A1
GENERAL INFORMATION:
APPLICANT: Lindner, Luther E.
APPLICANT: MacPhee, Rathleen
TITLE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026D
CURRENT APPLICATION NUMBER: US/09/894,467
CURRENT PILING DATE: 2001-06-28
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 20
SENGTH: 1208
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                                                      Gaps
13
                                    Length 1208;
                                                      Indels 24;
67
and
positions 40
                                   Score 904.8; DB 10;
Pred. No. 3.8e-236;
1; Mismatches 136;
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n located
; OTHER INFORMATION: nucleotide
; OTHER INFORMATION: unknown.
US-09-894-467-1
                                  Query Match 62.3%;
Best Local Similarity 86.7%;
Matches 1048; Conservative
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δδ .	8 8 8	vo Vo	oy B	40 40 40	OY DD	QY Db	Qy Db	oy Db	QY Dp	Qy Db	Qy Dp	O D	Qy Dp	OY OA	QY	Q7 Dp	& A &
Db 960 AAGGGGGACCTGGAGCAAATCCCGAAAAACCGTCTCAGTTGGGATTGCACTCTGCAACT 1019	OY 1233 CGAGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTT 1292 	OY 1293 CCGGGCCTTGTACACACCGCCGTCACACCATGGGAGTTGGTTCTACCCGACGACGNTG 1352	Oy 1353 GGTBACCTTCGGGGGGCAGGCGCCACGGTAGGATCAGCGACTGGGGTGAAGTCGTAAC 1412	Oy 1413 AAGGTAGCC 1421 	RESULT 9 US-09-847-513A-1 ; Sequence 1, Application US/09847513A	FUBLICATION NO. USZUJJU44/SAI GENERAL INFORMATION: APPLICANT: MBARI APPLICANT: DeLong, Edward	FIFTE OF INVENTIONS Light-driven energy generation using proteorhodopsin; FILE REFERENCE: MBA-101; CURRENT APPLICATION NUMBER: US/09/847,513A	CORRENT FILLING LATE: ZU01-03-01 PRIOR FILLING DATE: Z000-05-03 NUMBER OF SEQ ID NOS: 65 COURMANDER: LOCATION LOCATIO	,		OIRER INFORMATION: From Control of the Sequence. LOCATION: (1593)(2807) OTHER INFORMATION: Predicted threonine dehydratase. Contains 'n' at position 2753.	 FUBLICATION INFORMATION: FUBLICATION INFORMATION: AUTHORS: Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T., Hadd,A.,Nguyen,L.P., AUTHORS: Jovanovich,S.B., Gates,C.M., Feldman,R.A., DeLong,E.F. TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea 	OUTUME: SOLENCE SOLENCE SOLUTION SOL) DATE: 2000-9-15 ; DATABASE ACCESSION NUMBER: AF279106 ; DATABASE ENTRY DATE: 2000-06-15 ; RELEVANT RESIDUES: (50866)(51615)	Query Match 60.7%; Score 881.4; DB 11; Length 105184; Best Local Similarity 77.3%; Pred. No. 2e-229; Matches 1179; Conservative 0; Mismatches 272; Indels 75; Gaps 6;	STTTGATCCTGGCTCAGAACGAAGCTGGCGGCAGGCTTAACACATGCAAGTCCAGCGA 60 HIIIIII HIIIIII HIIII HIIIIIIIIIIIIIII	GCC 109 ACC 977

Ċ	Qy 269 G	DD 303 G	QY 329 G	Db 363 C	Qy 389 p	Db 423 P	Qy 423 C	DD 483	Oy 483 C	Db 543 C	Oy 543 #	Db 603	QY 603 C	D £99 qq	Qy 663 p	Db 723 #	Oy 723 1	Db 783 1	Qy 783 1	Db 843 1	Qy 843 (DP 805 C	Qy 903 C	Dp 962 (Oy . 963	•	Oy 1023	٠	Db 1141 7	Ov 1143 (Oy 1189	Db 1261 (Qy 1241.	Db 1321
	98923	1246	98983	1306	99043	1366	99103	1426	99163	qa	δδ	9G	δo .	qa			QC di	ES FOR			ξο <u> </u>	- T	άσ	. ·	; Length 1532;	Indels 82; Gaps 6;	09	62	102	122	162	787	208 242		
	DD 98864 AGTAGGGTACACACGTGCTACAATGGGAGATACAC	Qy 1189 TTAATCCCCAAAAGCCATCTCAGTTCGCATTGCCTCGCAACTCGAGGGCATGAAGT	Db 98924 GCTAATCCTAAAAGTCTTTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGT	Qy Tegaategetagtaategeggaacageatgeege	Db 98984 CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCTCGGGTCTTGTAC	_	Db 99044 ACACCCCCCCCCCACACACCCATGGAATTGCACCAGAAGTAGATAGTCTAACCTTAGGG	Oy 1367 GGGCAGGCGGCCACGTAGGATCAGCGACTGGGGT	Db 99104 AGGCCTTTACCACGGTGTGCTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGG	Qy 1427 GGAACCTGCGGCTGGATCACCTCCTT 1452	Db 99164 GGAACCTGTGGCTGGATCACCTCCTT 99189		MESULI 10 US-10-007-725-6 . Segment A hand destion HS // 0007725	Sequence o, Aprilcation 05/1000//25 Publication No. US20020150887A1	SENERAL INFORMATION: APPLICANT: Maruyama, Akihiko Applicant: Utanakikana makanat	APPLICANT: https://www.nichi.n	APFLICANI: Sunamura, Michinari ; APPLICANT: Kurane, Kyulchiro ; TITIE OF INVENTION: METHODE AND MICTET ACTD DEOD	; IIILE OF INVENTION: MEINCUS AND NOCHEL ACID F; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS; TITLE OF INVENTION: ENVIENMENTAL SAMPLES	; FILE REFERENCE: 13558-003001 . CIRDDENN ADDITORY MINDED.	CORRENT FILING DATE: 2001.11-07.	FAICH RELIGIOUS ACCUSATION OF STATE OF STATE OF STATE OF SECTION O	SOFTWARE: FastSEQ for Windows Version 4.0	; SECTH: 1532 ; TENGTH: 1532 ; TAVDE: DAA	ORGANISM: Cycloclasticus pugetii US-10-007-725-6	59,9%; Score 869.8;	Best Local Similarity 76.7%; Pred. No. 1.3e-226; Matches 1175; Conservative 1; Mismatches 274;	Qy 1 AGTTTGATCCTGGCTCAGAACGAACGCTGGCGGCAGGCTTAACACACATGCAAGTCGAGCAG	Db 3 AGTTGATCATGGCTCAGATTGAACGCTGGCGGCATGCCTAACACATGCAAGTCGAACGG	61 GACCTTCG	Db 63 AAACAGAATGCAGCTTGCTAGCAGGCGGTCGAGTGGCGGACGGGTGAGTTATGCATAGGA	103	123 ATCCGCCCGATAGTGGGGGACAA	OY 163 GGGGAAAGATTTATCGGAGAAGGATCGGCCCGCTTGGATTAGGT		QY 209 AGTTGGTGGGGTAATGGCCCACCAAGCGACGATCCATAGCTGGTTTGAGAGGATGATCA

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                                   AAAGCTCTTTCAGCTGGGAAGATAA---------TGACGGTAC
                            CTTACGGGTIGGGCTACACGTGCTACAATGGTGGTGACAGTGGG-----
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OY 395 CTTCAGCTGGGAAGATAATGACGGTACCAGCAGA 429	0 0 0 0 0 0 0 0 0 0	
0y 1301 TTGTACACACCGCCGTCACCATGGGAGTTGGTTCTACCCGACGACGTTACC 1360	FIGURE 11 10.007-735-5 Sequence 5, Application US/10007725 Publication No. US2002015087A1 APPLICANT: Mitamira, Athliko APPLICANT: Higashlara, Takanori APPLICANT: Higashlara, Takanori APPLICANT: Higashlara, Takanori APPLICANT: Higashlara, Takanori APPLICANT: Higashlara, Mitchinari APPLICANT: Sunamura, Mitchinari APPLICANT: Sunamura, Mitchinari APPLICANT: Sunamura, Mitchinari APPLICANT: Sunamura, Mitchinari APPLICANT: Namura, Relucia More Carlor PROBES FOR TITLE OF INVERTION: MOLECULAR CENETIC ANALYSIS OF POLLUTED ENVIRONMENTS FILE OF INVERTION: MUMBER: US/10/007,725 CURRENT FILING DATE: 2001-11.09 PRIOR PADATE: 2001-11.09 PRIOR FILING DATE: 2001-11.09 MUMBER OF SEQ IO WINDER: US/10/007,725 DRIOR FILING DATE: 2001-11.09 MUMBER OF SEQ IO WINDER: US/10/007,725 DRIOR FILING DATE: 2001-11.09 MUMBER OF SEQ IO WINDER: US/10/007,725 MUMBER OF SEQ ION WINDER: US/10/007,725 MUMBER OF SEQUENCE CONSERVE CONSECUENCE CO	Db 361 GGGGCAACCCTGATCCAGCCATGCCGCTGTGTGAAGAGGCCTTCGGGTTGTAAAGCA 420

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                  Sequence 1, Application US/09791592
Patent No. US20010021223A1
GENERAL INFORMATION:
APPLICANT: Canon Inc.
TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid
TITLE OF INVENTION: monomer unit, and method for producing the same.
FILLE REFERENCE: 4396021
CURRENT APPLICATION NUMBER: US/09/791,592
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 1
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Pred. No. 1.9e-224;
0; Mismatches 268;
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; ORGANISM: Pseudomonas jessenii 161
US-09-791-592-1
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Best Local Similarity 77.1%;
Matches 1157; Conservative
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RESULT 12
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අු	722 ATTAACCTAATACGTTAGTGTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGT 481	; Sequence 1, Applicat : Patent No. 1152002002
Qy	451 GCCAGCAGCCGGGTAATACGGAGGGGCTAGCGTTGTTCGGAATTACTGGCCGTAAAGC 510	GENERAL INFORMATION:
අ	482 GCCAGCAGCGGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGC 541	TITLE OF INVENTION:
ν .	511 GCACGTAGGCGGACTGGAAAGTCAGGGGAATCCCAGGGCTCAACCTTGGAACTGCCT 570 511 GCACGTAGACTGCAAAGTCAAGTGAATCCCAGGGCTCAACCTTGGAACTGCCT 570 512 GCACGTAGAACTGCAAAGTCAAGTGAAAAAAAAAAAAAA	; FILE REFERENCE: 43; CURRENT APPLICATION
3	1,000,000,000,000,000,000,000,000,000,0	NUMBER OF SEQ ID NO
දු ද	571 IIGAAACIATCAGICIGGACIICGAGAGAGAGAGATTCCGAGIGIAGAGGTGAA 630 1	; SEQ ID NO 1 ; LENGTH: 1501 . TVPE: DNA
ò	TTCGTAGATATTCGGAGGAACACCAGTGGCGAAAGGCGGCTCACTGGATACTGACGC	; ORGANISM: Pseudomo US-09-748-205-1
qq		Query Match
, 0	691 TGAGGTGCGAAAGCGTGGGGAACAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA 750	Best Local Similarit Matches 1157; Conse
q	722 TGAGGTGCGAAAGCGTGGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA 781	Oy 22 GAACGCTG
ογ	751 CGATGAATGCCAGACGTCGCCAAGCATGCT-TGTCGGTGTCACCACACACGATTAAGCA 809	DD 2 GAACGCTG
qq	782 CGATGTCAACTAGCGTTGGGAGCCTTTGAGTGGCGCGCAGCTAACGCATTAAGTT 841	Qy 74AGCG
δλ	810 TICCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCAC 869	DD 62 ATTCAGCG
qq	842 GACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCAC 901	QY 130 GGGAAACT
ò	870 AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAACCCTTGACA 929	Db 122 TCGAAAGG
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ďδ	990 GGCTGTCGTCGTCGTCGTGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCAC 1049	Db 242 CGACGATC
q	1022 GGCTGTCGTCGTCGTGTGTGTGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTT 1081	Qy 296 GACTCCTA
Qy	1050 GICCCTAGITGCCAGCAATTCA-GTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGG 1108	Db 302 GACTCCTA
q	1082 GTCCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAACTGCCGGTGACAAACCGG 1141	Qy 356 AIGCCGCG
Qy	1109 AGGAAGTGTGGATGACGTCAAGTCCTCATGGGCCTTACGGGTTGGGCTACACACGTGCT 1168	Db 362 ATGCCGCG
원	1142 AGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCT 1201	Qy 411
ογ	1169 ACAATGGTGACAGTGGGTTATCCCCAAAAGCCAT 1206	Db 422 ATTAACCT
q	GTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCA	Oy 451 GCCAGCAG
δō	1207 CTCAGTTGGGATTGTCCTCTGCGAGGGCATGAAGTTGGAATGGCTAGTAATGGG 1266	Db · 482 GCCAGCAG
୍ ପ୍ର	1262 CGTAGTCCGGATCGCAGTCTGCAACTCGACTGGCTGAAGTCGGAATCGCTAATCGCG 1321	Oy 511 GCACGTAG
δ	1267 GAACAGCATGCCGCGGAATACGTTCCCGGGCCTTGTACACACCGCCGTCACACCATG 1326	Db 542 GCGCGTAG
q	1322 AATCAGAATGICGCGGTGAATACGTICCCGGGCCTIGTACACACCGCCCGTCACACCATG 1381	Oy 571 TTGAAACT
. Оу	1327 GGAGTTGGTTCTACCCGACGACGACGCTAACCTTCGGGGGGCAGGCGCCACGGTAG 1386	Db 602 TCAAACT
qq	1382 GGAGTGGGTTGCACCAGAAGTAGCTAGCTACCTTCGGGAGGACGGTTACCACGGTGTG 1441	Oy 631 TTCGTAGA

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7: Polyhydroxyalkanoate its manufacturing method, and microorga
is those are used for the method.
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1387 ATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1446
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y 121 AATAGCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTATCGG 180	181 AGAAGGATCGGCCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACG 24	241 ATCCATACTGGTTTGAGAGGATGATCAGCACACTGGGACTGAGACACGGCCCAGACTC 30 241 ATCCATAGTTGAGAGGATGATCAGCACACACGGGACGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCCAGAGACTCCAGACTCGAGACTCGAGACTCGAGACTCGAGACTCGAGACTCAGACTCAGACTCAGACTCAGAACTCAGACTCAACTCAGACTCAGACTCAGACTCAGACTCAGACTCAACTCAGACTCAACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTCAACTCAGACTCAA	301 CTACGGGAGCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCC 3 CTACGGGAGCAGCCAGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCC 3 CTACGGGAGGCAGCAGTGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCAATGGGGGCCAACCTGATCTAGCCAATGGGGGCAACCTGATCTAGCATGG	361 GCGTG 	Y 421 ACCAGCAGAAGAAGCCCGGGTAACTCCGTGCCAGCAGCGGGGTAATACGGAGGGGCT 480	y 481 AGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTG 540	y 541 AAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGG 600	y 601 GTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGC 660	y 661 GAAGGGGGCTCACIGGCTCGATACIGACGCTGAGGTGCGAAGCGTGGGGAGCAAACAGG 720	y 721 ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT 780	19 781 IGECGGTGTCACACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAA 840 1	y 841 AACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGC 900	y 901 AACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCT 960	y 961 CGTAAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTCGTGTGTGT	y 1021 GGTTAAGTCCGGCAACGCGAACCCACGTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080	y 1081 TCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGAGGTGTGGATGACGTCAAGTCCTCATGG 1140	1141 GCCTTACGGGTTGGCCTACACGTGCTACAATGGTGGTGACAGTGGGTTAATCCCCAAA 1200	y 1201 AGCCATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
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OY 1021 GGTTAAGTCCGGCAACGAGCGCACGTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080	TCTATGGAAACIGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGG 114	GCTTACGGGTTGGGCTACACGTGCTACAATGGTGACAGTGGGTTAATCCCCAAA 120	1201 AGCCATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 126 1201 AGCCATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 126	OY 1261 ATGGGGAACAGCATGCCGGGGGAATACGTTCCCGGGCCTTGTACACACGCCGTCAC 1320	Oy 1321 ACCATGGGAGTTGCTTCTACCGGACGACGATGCGTTCGGGGGGCAGCGGCCAC 1380 Db 1321 ACCATGGGAGTTGGTTCTACCCGACGACGACGATTCGGGGGGCAGGCGGCCAC 1380	OY 1381 GGTAGGATCAGCGACTGGGGTGAAGTACCATAGCTAGCCGTAGGGGAACCTGCGGCTG 1440	Oy 1441 GATCACCTCTT 1452	RESULT 2 US-10-049-228-1	; Sequence 1, Application US/10049228 ; GENERAL INFORMATION: ; APPLICANT: TSUBOKURA, Akira ; APPLICANT: MIZUTA, Haruyoshi	; FILEE REFERENCE: 3831-0003 ; FULE REFERENCE: 3831-0003 ; CURRENT APPLICATION NUMBER: US/10/049;228 ; CURRENT FILING DATE: 2002-02-11	FALON REPLICATION NOMBER: PCIVIOUS 48,4 PRIOR FILING DATE: 2001-06-08 PRIOR APPLICATION NUMBER: JP 2000-175124 PRIOR FILING DATE: 2000-06-12	WORDER OF SEQ ID NOS: 2 SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 1 ; IENGEL 1452	ORGANISM: Unknown FEATURE: OTHER INFORMATION! Nucleotide sequence corresponding to the 16S ribosomal RNA of E-3) VAREX INFORMATION: 9. SIGNIN) LOCATION: (1350)(1350) ; OTHER INFORMATION: n 1s A, C, G or T	Ouery Match Query Match Best Local Similarity 100.0%; Score 1451; DB 44; Length 1452; Best Local Similarity 100.0%; Pred, No. 0; Matchee 1452. Concernative On Mismatchee	CIGGCICAGAACGAACGCGGCAGCAITAACACATGCAA	61 GACCTTCGGGTCTAGCGGGGGGGGGGGGGGGGGGGGGGG	ol GACCITCGGGICTAGCGGGGGGGGGGGGGGGGGGGGGGGG

361 GGGTGAGTGATGAAGGCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGT 420	601 GTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGC 660	721 ATTAGATACCTGGTAGTCCACGCCGTAAACGATGAATGCAGACGTCGGCAAGCATGCT 780	841 AACTCAAAGGAATTGACGGGGCCCCACAAGCGGTGGACATGTGGTTTAATTCGAAGC 900	961 CGTAAGACTGCACACAGGTGCTGCATGGCTGCTCGCTCGTGTGGTGGATGTTC 1020	1 TCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGGGATGACGTCAAGTCCTCATGG 114	1	1261 ATGGGGAACAGGATGCGGGGGAATACTTCCGGGGCTTGTACACGGCGCGGTAC 1320 [111]	1379 ACGGTAGGATCAGCGACTGGGGTGAACTGTAACAAGGTAGCC 1421
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	<pre>/y 1441 GATCACCTCCTT 1452 bb 1441 GATCACCTCCTT 1452 seguence 2, Application US/10049228</pre>	APPLICANT: TSUBOKURA, Akira APPLICANT: TSUBOKURA, Haruyoshi TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS TITLE OF INVENTION: PROCESS OF OF STATE OF S	PRIOR APPLICATION UNUBER: 2000-175124 PRIOR APPLICATION UNUBER: 92 2000-175124 PRIOR FILING DATE: 2000-06-12 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin version 3.1 SEQ ID NO 2 LENGTH: 1426 TYPE: DNA	FORMALISM: UNKNOWN. FRATURE: OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA of A-5 OTHER INFORMATION: 81-1 strain IS-10-049-228-2 OURTY MATCh ODER A. Score 1380; DB 44; Length 1426;	° \$=\$		181 AGAAGGATCGGCCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACG 240	301 CTACGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCC 36

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GGCTGTCGTCAGCTCGTGTGTGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCAC 1049
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APPLICANT: BRETZEL, Werner
APPLICANT: BRETZEL, Werner
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: PELISEY, Alexel
APPLICANT: PELISEY, Alexel
APPLICANT: PELISEY, Alexel
APPLICANT: WELSEY, Alexel
APPLICANT: WELSEY, Alexel
APPLICANT: WELSEY, Alexel
TITLE OF INVENTION: IMPROVED ISOPRENOID PROD
FILE REFERENCE: C38435/121966
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PATENTING DATE: 2001-06-06
SOFTWARE: PATENTING DATE: 1901-06-06
SEQ ID NOS: 197
SERVICENTING DATE: 1001-06-06
SECONDO 12
SERVICENTING DATE: 1001-06-06
SECONDO 12
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                                                                                                        APPLICANT: YELISEEV, Alexel A.
TITLE OF "INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                 Score 1285.2;
Pred. No. 0;
0; Mismatches
Sequence 12, Application US/10166225A GENERAL INFORMATION:
                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Paracoccus sp. R-1512
US-10-166-225A-12
                                             APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: LOPEZ-ULIBARRI, RUAI
APPLICANT: MAYER, Anne F.
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Best Local Similarity 95.6%;
Matches 1343; Conservative
                                APPLICANT: BERRY, Alan
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SEQ ID NO 12
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9	best Local Similarity 93.0%; Frec. No. U; Matches 1343; Conservative 0; Mismatches 59; Indels 3; Gaps 2;	30 GCGGCAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGGGGGGGG	90 GTAACGCGTGGGAACGTGCCCTTCTCTACGGAATAGCCCCGGGAAACTGGGAGTAATACC 149	61 GTAACGCGTGGGAACGTGCCTTTGCTACGGAATAGTCCCGGGAAACTGGGTTTAATACC 120	150 GTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAGGATCGGCCCGCGTTGGATTAGGTA 209 	GTTGGTGGGGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTTGAGAGGATGATCAG	181 GITGGTGGGGTAATGGCCTACCAAGCCGACGATCCATAGCTGGTTGGGTGGG		ACAATGGGGGAACCCTGATCTAGCCATGCGGGTGAGTGATGAAGGCCTTAGGGTTGTA	301 ACAATGGGGGGAACCCIGATCIAGCCATGCCGGTGAGTGATGAAGGCCCTAGGGTTGIA 350 390 AAGCTCTTTGAGCTGGGAAGATAATGACGGTAACAGAGAAGAAGAAGAGCCCCGGGTAAGTGCG 449	61 AAGCTCTTCAGCTGGGAAGATAATGACGGTACCAGCAGAAGAAGCCCCGGCTAACTCCG	50 TGCCAGCAGCGCGCGGTAATACGGAGGGGCTAGCGTTGTTCGGAATTACTGGGCGTAAAG	TGCCAGCAGCCGCGGTAATACGGAGGGGCTAGCGTTGTTCGGAATTACTGGGCGTAAAG	510 CGCACGTAGGCGGACTGGAAGTCAGAGGTGAAATCCCAGGGCTCAACCTTGGAACTGCC 569 [570 TITGAAACTAICAGICIGGAGITGAGAGAGGIGAGIGGAAIICCGAGIGIAGAGGGGAA 629 [1	ATTCGTAGATATTCGGAGGAACACCAGTGGCGAAAGGCGGCTCACTGGCTCGATACTGACC	601 AITCGIAGATAITCGGIGGAACACCAGIGGCGAAGGCGGCTCACIGGCTCGAIACTGACG 660	690 CTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAGCCGTAA 749 	750 ACGATGAATGCCAGACGTCGCAAGCATGCTTGTCGGTGTCACCTAACGGATTAAGCA 809 	TTCCGCCTGGGGGGTACGGTCCCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCAC	781 TICCGCCTGGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCAC 840	AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGGAAACCTTACCAACCCTTGACA	AAGCGGIGGAGCAIGTGGTTIAAITCGAAGCAACGCGCAGAACCTIACCAACCCTIGACA 90	930 TGGCAGGACGCTGGAGAGATTCAGCTTTCTCGTAAGAGCCTGCACAGAGGTGCTGCAT 989 11 1 1 1 1 1 1 1 1 1	GGCTGTCGTCAGCTCGTGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCAC	961 GGCTGTCGTCGTCGTGTCGTGAGTTCGGTTAAGTCCGGGAACGCGCAACCCAC 1020	1050 GTCCCTAGTTGCCAGCAATTCAGTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGGA 1109
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of Unknown Organism: Paracoccus sp equence of 16S rDNA corresponding to strain EMB d Fragments for the Identification of Bacteria Wastewater Bloreactors GCAGGCGCCACGGTAGATCAGCGACTGGGGTGAAGTC 1407 GGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTG 256 CACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG 316 AATCCCCAAAAGCCATCTCAGTTCGGATTGTCCTGCA 1229 SICCICAIGGGCCITACGGCITGGGCTACACACGTGCTA 1169 ATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATAC 1289 GTTGGGCACTCTATGGAAACTGCCGATGATAAGTCGGA 1079 4; Gaps DB 32; Length 1385; 85; Indels Score 1212.6; Pred. No. 0; Mismatches AACC 1432 ||||| AACC 1404 9/735,567 1,140 67

oy.	317 TGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCCGCGTGAGTGA	. vo aa	1395 CTGGGG 1400 6 CTGGGG 1
. qg	377.CCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGACGGTACCAGCAGAAGAAGC 436 	RESULT 7 US-60-171 ; Sequenc	SULT 7 -60-171-140-1/c -60-171-140-1/c
δ da	437 CCGGCTAACTCCGTGCCAGCCGCGGTAATACGGAGGGGGCTAGCGTTGTTCGGAATT 496 ,	APPLIC TITLE	DE INVENTION: Michael OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in OF INVENTION: Industrial Wastewater Bioreactors
Qy Dp	497 ACTGGGCGTAAAGGGCACGTAGGGGGACTGGAAAGTCAGAGGTGAAATCCCAGGGCTCAA 556 	CURREI CURREI NUMBER	RENCE: BCI033 US PPLICATION NUMBER: ILING DATE: 1999-1
oy Ob	557 CCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGGGAGTGCGA 616 	SOFTWAKE: SEQ ID NO 1 LENGTH: 1 TYPE: DNA	OFFWARE: MICROSOIT OILIGE 9/ DENOTH: 1385 TYPE: DNA
y d	617 GTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCTCACTGG 676 	CRGANISM CREATURE: COTHER IN FEATURE:	LOM: Unknown Organism RE: INFORMATION: Description of Unknown Organism: Paracoccus sp RE:
S G	677 CTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTA 736 	; OTHER INF US-60-171-140 Query Match	N N
& 8	737 GTCCACGCCGTAAACGATGAATGCCAGACGCAAGCATGCTTGTCGGTGTCACACCT 796 	Best Lo Matches	Best Local Similarity 93.6%; Pred. No. 0; Matches 1297; Conservative 0; Mismatches 85; Indels 4; Gaps 3; 18 GAACGAACGCTGGCGGCATAACACATGCAAGTCGAAGCGAGACTTCGGGTCTAGCG 77
, y 4	AACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCCAAAGGATTGA	ි සි සි	
i . A	CGGGGCCCGCACACGCTGCACCATGTGCTTTAATTCGAAGCACGCGCAGAACCTTA	ž a	GCGGACGGGTGACCCTTGCCCTTTCGGAATAGCCCTGGGAAACT
g '9' g	343 CGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCAGAACCTTA 486 917 CCAACCCTTGACATGGCAGGACGGCTGGAGATTCAGCTTTCTGGTAAGAGACCTGCAC 976	Э	138 GGRAGTAATARCGETTATGGGGGAAAGATTATGGGAGAGAGAGGGGGGGGGG
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9 · V		λο O	257 AGAGGATCATCAGCCACACTGGGATTGAGACACGGCCCAGACTCCTAGGGGAGGCAGCAG 31b
ga, ko	365 GAGCGCAACCCACACTTCCAGTTGCCATC-ATTCGGTTGGGCACTCTGGAAGTGCCG 307 1097 ATGATAAGTCGGAGGAAGGTGGATGACGTCACAGTCCTCATGGGCTTACGGGTTGGGC 1156	Qa	317 TGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCCATGCGGTGAGTGA
d y	306 ATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGCCCTTACGGGTTGGGC 247 1157 TACACACGTGCTACAATGGTGACACAGGGTTAATCCCCAAAAGCCATCTCAGTTCGG 1216	QQ .	377 CCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGTACCAGCAGAAGAAGCC 436
d ç	246 TACACACGTACAATGGCGGTGACAATGGGTTAATCCCAAAAAGCCGTCTCAGTTCGG 187 1217 ATTGTCCTCTGCAAGTGGGATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATG 1276	δο d	437 CCGGCTAACTCCGTGCCAGCCGCGGTAATACGGAGGGGGCTAGCGTTGTTCGGAATT 496 111111111111111111111111111111111111
ପୁର ଓ	186 ATIGGGGTCTGCAACTCGACCCCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATG 127 , 1277 CCGCGGTGAATACGTTCCCGGGCTTGTAATACGTTCCCGGGCCTTGTAAACACCGCCCGGTCAACAGTTGGTAATACGTTCCCGGGCCTTGTAAACACCCCCCGGTCAACAATACGTTCCCGGGCCTTGTAAAACACCGCCCGGTCAACAACAATACGTTCCCGGGCCTTGTAAAAAACAACAACAAAAAAAA	č d	497 ACTGGGCGTAAAGGGCACGTAGGCGGACTGGAAAGTCAGAGGTGAATCCCAGGGCTCAA 556 11111111111111111111111111111111111
୍ ପ _ର ୍		. AO	7 CCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGTGAGTGGAATTCCGA
ž d	1337 CTACCCGACGACGATGCGCTAACCTTCGGGGGGCAGGCGGCCACGGTAGGATCAGCGA 1394 	g &	845 CCCCGGAACTGCCTTCAAAACTGTCAGTCTGGAGTTCGAGAGAGA

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Query Match 76.7%;
Best Local Similarity 87.1%;
Matches 1288; Conservative
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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                                                             GTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCTTGTCGGTGTCACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR APPLICATION NUMBER: US 09/514,000 NUMBER OF SEQ ID NOS: 13351 SEQ ID NO 191 LENGH 20310
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; ORGANISM: Agrobacterium
US-09-739-449-191
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                                                                        1 AGTITGAICCIGGCICAGAACGAACGCIGGCGCCAGGCTTAACACATGCAAGTCGAGCGA
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                                     Gaps
                                    29;
Length 20310;
                                     Indels.
 Score 1113; DB 32;
Pred. No. 0;
0; Mismatches 161;
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GTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTGG 1076 	oy oy	. 92 4
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	y d	661 GAAGGCGGCTCACTGGCTCGATACTGACGTGAGGTGCGAAAGCGTGGGGAGCAAACAGG 720
	\$ G	721 ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT
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	\$ 6 6	841 AACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGACCATGTGGTTTAATTCGAAGC 900
	oy Op	901 AAGGGGAGAACCITACCAACCCITGACAT GGCAGGACCGCTGGAGAATTCAGCT 956
	oy D	957 TECTEGRAAGACETGCACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGGAAT 1
Length 20310;	oy Dp	1017 GTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTGG 107. 111
SCAAGTCGAGCGA 60	oy Op Op	1077 GAACTCTAIGGAAACTGCCGAIGAFAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCCT 1135
CGG 12	oy Dp	1136 CATGGGCCTTACGGGTTGGGCTACACGTGCTACATGGTGGTGACAGTGG 1187
00-00-00-00-00-00-00-00-00-00-00-00-00-	oy Db	1188GTFAATCCCCAAAGCCATCTCAGTTCGGATGTCCTCTGCAACTCG 1234
ACG 24	ογ	1235 AGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTTCC

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PCT-US98-23674-2/c
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                                      CCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAGG
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                                                                                                                            Sequence 12, Application US/09726774
GENERAL INFORMATION:
JAPPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Antisense Antibacterial Method and
TITLE OF INVENTION: Composition
FILE REFERENCE: 0450-01032.30
CURRENT APPLICATION NUMBER: US/09/726,774
CURRENT FILING DATE: 2000-11-29
FRIOR APPLICATION NUMBER: US 60/168,150
FRIOR PILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1466
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Pred. No. 0;
0; Mismatches
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LOCATION: (1)...(1466)
OTHER INFORMATION: n = A.T.C or
US-09-726-774-12
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Bartonella henselae
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Best Local Similarity 87.1%;
Matches 1278; Conservative
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US-09-726-774-12
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APPLICANT: MacPhee, Kathleen
TITLE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026FCT
CURRENT APPLICATION NUMBER: PCT/US98/23674A
CURRENT FILING DATE: 1998-11-06
EARLIER RPLING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 20
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PCT-US98-23674-2/c
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                                                                                                                                                                                                                                                                                                                     Length 1502
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Pred. No. 0;
0; Mismatches 177;
                           APPLICANT: Lindner, Luther'E.
APPLICANT: MacPhee, Kathleen
TITLE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026PCT
CURRENT APPLICATION NUMBER: PCT/US98/23674A
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/064,472
EARLIER FILING DATE: 1997-11-06
NUMBER QF SEQ ID NOS: 20
SEQ ID NO 2
 Sequence 2, Application PC/TUS9823674A
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86.2%;
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Best Local Similarity
Matches 1245; Conserv
                 GENERAL INFORMATION:
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Unknown
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GGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGG 319
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GENERAL INFORMATION:
APPLICANT: Lindner. Luther E.
APPLICANT: MacPhee, Kathleen
ITILE OF INVENTION: Human Blood Bacterium
FILE REFERENCE: D6026D
CURRENT APPLICATION NUMBER: US/09/894,467
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/187,946
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.8%;
Best Local Similarity 86.2%;
Matches 1245; Conservative
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US-09-894-467-2/c
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                              GAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAGGATCGGCCCGCGTT
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Best Local Similarity 00.22
Matches 1245; Conservative
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q	1082 GCTAACTTCGTGCCAGCAGCGGGGAATACGAAGGGGGCTAGCGTTGCTCGGAATCACT 1023	ທຣ-09. ; Sequ	-900-876-2 uence 2, Ap
ŏ	500 GGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAATCCCAGGGCTCAACCT 559	; GENI	ERAL INFORM PLICANT: WA
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ογ	560 TGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGTGGAATTCCGAGTG 619	: :	ILE OF INVE LE REFERENC
Q	962 CAGAATGGCCTTCGATACTGGGACGCTWGAGTATGGTAGGTTGGAGTGGACTGCGAGTG 903		RRENT APPLI RRENT FILIN
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đ	902 TAGAGGTGAAATTCGTAGATATTCGCAAGAACACCGGTGGCGAAGGCGGCCAACTGGACC 843	SOS	FIWARE: Pat
δ	680 GATACTGACGCTGAGGGGAAAGCGTGGGGAAAACAGGATTAGATACCCTGGTAGTC 739		LENGTH: 1490
QQ	842 ATTACTGACGCTGAGGCGCGGAAACGTGGGGGGGGCAACAACAGGATTAGATACCTGGTAGTC 783		RGANISM: Rh
δy	740 CACGCCGTAAACGATGAATGCCAGACGTCGCGAAGCATGCTTGTCGGTGTCACACCTAAC 799	Z Z)	EATORE: AME/KEY: mi
đ	782 CACGCCGTAAACGATGAATGCCAGCTGTTGGGGTGCTTGCACCGCAGTAGCGAGCTAAC 723	36; 	CATION: (1
ογ	800 GGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGG 859	Z 1 7	LOCATION: (7
୍ପ	722 GCTTTGAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGG 663	5 Z }	NAME/KEY: mi
οy	860 GGGCCGGCAAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGGAGAACCTTACCA 919		COCATION: (BOTHER INFORM
QQ	662 GGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACACGCGCAGAACCTTACCA 603		AME/KEY: MI OCATION: (4
ΟŸ	920 ACCCTTGACATGGCAGGACGCTGGAGAGATTCAGCTTTCTCGTAAGAGACCTGCACACA 979	5 Z .	NAME/KEY: mi
ф ,	602 TCCTTTGACATGGCGTGTTACCCAGAGAGATTTGGGGTCCACTTCGTGGCGCGCACACA 543	102	· Œ. ·
ογ	980 GGTGCTGCATGGCTGTCGTCGTCGTGCTGAGATGTTCGGTTAAGTCCGGCAACGAC 1039	ž 11 č	LOCATION: (5
QQ	542 GGIGCIGCATGGCIGICGICACGCICGIGAGAIGITGGGITAAGICCCGCAACGAG 483		NAME/KEY: mi
Oy	1040 CGCAACCCACGTCCTAGTTGCAGCAATTCAGTTGGGAACTCTATGGAAACTGCCGATG 1099	102	OTHER INFORM
đ	482 CGCAACCÇACGICCIIAGIIGCCAIC-AIICAGIIGGGCACICIAGGGAGACIGCCGGIG 424		LOCATION: (8
ογ	1100 ATAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCCTCATGGGCCTTACGGGTTGGGCTA 1158		NAME/KEY: mi
đ	423 ATAAGCCGCGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGCCCTTACGGGATGGGCTA 364	0.	
ογ	1159 CACACGTGCTACAARGCTGGTGACAGTGGGTTAATCCC 1197	: A C	LOCATION: (9
අු	363 CACACGIGCIACAAIGGCGGIGACAGIGGGACGCGAAGGAGCGAICTGGAGCAAAICCCC 304		NAME/KEY: m1
δo	.1198 AAAAGCCATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGGGATGAAGTTGGAATCGCTA 1257	102	OTHER INFORM
q	303 AAAAGCCGTCTCAGTTCGGATTGCACTCTGCAACTCGAGTGAAGGCGGAATCGCTA 244	,	LOCATION: (1
å i	GTAATCGCGGAACACCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCT 13:		NAME/KEY: mi
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λō	1318 CACACCATGGGAGTTGGTTCTACCCGACGACGATGCGTTACGGGGGGGG		LOCATION: (1 OTHER INFORM

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2, Application US/09900876

INFORMATION:

TT: WATANABE, KATSUJI

TT: WATANABE,

INVENTION: METHOD AND SYSTEM FOR SEARCHING FOR RELATIONSHIPS BETWEEN BI
INVENTION: IN GENES

TRENCE: 210847USOX

APPLICATION NUMBER: US/09/900,876

FILING DATE: 2001-07-10

FILING DATE: 2000-07-14

INTO DATE: 2000-07-14 ACGGTAGGATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGG 1437 NAME/KEY: misc_feature
LOCATION: (1332)..(1333)
OTHER INFORMATION: n = c, g, a, or t
NCME/KEY: misc_feature
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OTHER INFORMATION: n = c, g, a, or t a, or t Nodospirillum salexigens nisc_feature (596)..(596) RMATION: n = c, g, a, or ö or ö ö ö ö ö or ö ö (485)..(485) PRMATION: n = c, g, a, o misc_feature (490)..(490) PRMATION: n = c, g, a, o nisc_feature (1045)..(1045) RMATION: n = c, g, a, a, á (988)..(988) WATION: n - c, g, a, 72)..(73) MATION: n = c, g, á á ģ ģ è (875)..(876)
RMATION: n = c, g (1)..(1)
RMATION: n = c, g
misc_feature (709)..(709) RMATION: n = c, 9 misc_feature (828)..(828) RMATION: n = c, 9 (910)..(911) RMATION: n = c, g misc_feature ò misc_feature (85)..(85) isc_feature 13c_feature isc_feature isc_feature TGGA 1442 11111 CTGGA 59

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1388 CTAACCCGAAAGGGGGGCGANCGCCACGGTCAGGTCAGCGCACTGGGGTNNNNNGTAAC 1447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bower, Stanley G.
APPLICANT: Bower, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequencës and uses thereof FILE REFERENCE: 38-10(1586)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR PILICATION NUMBER: US 60/252,455
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO STR
                                                                                                                                                                                                                                                                                           CGGGCCTTGTACACACCGCCGTCACACCATGGGAGTTGGTTCTACCCGACGACGACGGCGTGCGGCGTTGTTCTTACCCGACGACGACGACGGGGGAGTTGGTTTTACACCGACGACGTGGAGAGACGGTTTGACCCGAAGACGGTGAG
                                                                                                 GGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCT
                                                                                                                                                                                                      CTGCGAGGGTGAGCGGAATCTCTAAAAGCCGTCTCACATTCGGATGTTCTCTGCAACTCG
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 TGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTG
                                                                                                                                                                                                                                          -----GIGGGTTAATCCCCAAAAGCCATCTCAGTTCGGATTGTCCTGCAACTCG
                                   TITCICGIAAGAGACCIGČACACAGGIGCIGCAIGGCIGCGICGICAGCICGIGIGGAGA
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                                                                                                                                                                                       CATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGGTGGTGACA-
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Pred. No. 3.1e-302;
0; Mismatches 199; Indels
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US-10-015-127-578
Sequence 578, Application US/10015127
GENERAL INFORMATION:
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US-10-015-127-578
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Best Local Similarity 84.6%;
Matches 1252; Conservative
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                                                                                                                                                      AGTITGATCCTGGCTCAGAACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCG-
                                                                                                                              Gaps
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                                                                                                   Score 1044.6; DB 38;
Pred. No. 6.1e-303;
0; Mismatches 208;
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ilarity 83.9%;
Conservative
NAME/KEY: misc_feature

LOCATION: (1437). (1442);

OTHER INFORMATION: n = c, g,

NAME/KEY: misc_feature

LOCATION: (1451). (1475);

OTHER INFORMATION: n = c, g,

US-09-900-876-2
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Matches 1941;
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	179 GGAGAAGGATGGCCGGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGA 	99 CGATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGAC	299 TCCTACGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGGAACCCTGATCTAGCCATG	359 CCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACG 	419 GTACCAGCAGAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGTAATACGGAGGGGG 	479 CTAGCGTIGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGGGGCGGACTGGAAGTCAGAGG 	539 TGAAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAG 	599 AGGTGAGTAGAATTCCGAGTGTACAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTG 	659 GCGAAGGCGCTCACTGGCTCGATACTGAGGCTGAGAAAGCGTGGGGAGAAACA	719 GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGAGGTCGGCAAGCAT- 	778 GCTTGTCGGTGTCACACCCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGAT 	838 TAAAACTCAAAGGAATTGACGGGGCCCCCACAAGCGGTGGAGCATGTGGTTTAATTCGA 	898 AGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGGAGGATTCAGC 	956 TITCTCGTAAGAGACCTGCACACAGGTGCTGCATGCCTGTCGTCAGCTGCTGTCGTGAGA 1	16 TGTTCGGTTAAGTCCGGCAACGAGCGCAAGTCCCTAGTTGCCAGCAATTCAGTTG	76 GGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGGGTG	36 CATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGGTGGTGGCAGGG	88GITAATCCCCAAAAGCCATCTCAGTTGGGATIGTCCTCTGCAACTCG
Db 16409	Oy 179 Db 16469	Oy % 239 Db 16529	Qy 299 Db 16589	Oy 359 Db 16649	Qy 419 Db 16709	Oy 479 Db 16769	Qy 539 Db 16829	Oy 599 Db 16889	Qy 659 Db 16949	Qy 719 Db 17009	Qy 778 Db 17069	Qy 838 Db 17129	Qy 898 Db 17189	Qy .956 Db 17249	Qy . 1016 Db 17309	0y 1076 Db 17368	Qy 1136 Db 17428	Qy 1188

Search completed: July 28, 2003, 12:52:47 Job time : 4126 secs

Appl Appl Appl Appl

Appl Appl Appl Appl \pp]

Perfect score:

Title:

Sednence:

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Run on:

OM nucleic į, Scoring table:

Total number

Searched:

Database :

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Sequence 198, P
Sequence 3550,
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Sequence 3531,
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  Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 158, Application US/09655378A
GENERAL INFORMATION:
GENERAL INFORMATION:
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDED ADDRESS:
CORRESPONDED & CARROLL
STREET: 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/655,378A
FILING DATE: 05-Sep-2000
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                US-10-323-069A-91
US-10-323-069A-90
US-10-323-069A-98
US-10-323-069A-93
US-10-367-793A-198
US-10-367-793A-3550
US-10-367-793A-3550
US-10-367-793A-3550
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                                           US-10-305-273B-106
US-10-367-793A-201
US-10-365-273B-86
US-10-323-069A-86
US-10-323-069A-94
US-10-323-069A-94
US-10-323-069A-99
US-10-323-069A-89
US-10-323-069A-87
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NAME: CARROLL, PETER G
REGISTATION UNBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 705-810
TELEFAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID
US-09-655-378A-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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478.6
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Sequence 3053, Ap
Sequence 12, App
Sequence 12, Appl
Sequence 2844, Appl
Sequence 2844, Appl
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2994, Ap
2995, Ap
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3357, Ap
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18, Appl
19, Appl
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69, Appl
                                                                                                                                                                 July 28, 2003, 09:25:08; Search time 166 Seconds (without alignments) 2162.994 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

(cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-367-794A-2845
US-10-367-794A-2944
US-10-367-794A-2944
US-10-367-794A-2994
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US-10-367-793A-3357
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US-10-305-273B-56
US-10-305-273B-57
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PCT-US03-20082-16
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US-10-305-273B-69
US-10-367-793A-326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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839.4 8828.6 8828.6 776.8 776.8 7113.6 7113.6 7113.6 7113.6 7113.6 7113.6 6699.4 6699.4 6662.6 6662.6 6662.6 6662.6

Result

1150 1150 1143 1210 1270	Oy 1241 TGAGGTTGGAATCGCTAC Db 1330 TGAGGTCGCAATCGCTAC OY 1301 TTGTACACACGCCCGTC OY 1301 TTGTACACACGCCCGTC OY 1361 TTCGGGGGCAGCCCCGTC OY 1361 TTCGGGGGCAGCGCCCGTC OY 1361 TTCGGGGGCCAGCCCCGTC OY 1361 TCGGGGGCCTTACC OY 1421 CGTAGGGAACCTGCGCC Db 1510 CGTAGGGAACCTGCGGCCTTACCCCCCCCTCCCCCCCCCC	Μα	Usery Match S7.18, Ouery Match S1.18, Best Local Similarity 76.68, Matches 1106; Conservative QY GGGGTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
10 AGTITGATCATGGCTCAGATTGAACGCTGGCGCGGCGGGCGTGACATGCAAGTCGAACGG 69 61 GACCTTCGGGTCTAGCGGCGGGGGGGTGAGTAACGCGTGGGA 102 61	209 AGTTGGTGGGGTAATGGCCCACCAAGCCGATCCATAGCTGGTTTGAGAGGATGATCA 268	424 AGCAGAAGAAGCCCGGGTAACTCCGTGCCAGCAGCGGGTAATACGGAGGGGCTAGC		114461CCGCGCGGAACCCTTATCTTGTTGCCAGCGGTCCGGCGGGAACTC 114
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sity of Science and Technology ULING COMPOSITION AND METHOD OF PRODUCTION THEREOF TCACACCATGGGAGTTGGTTCTACCCGACGACGNTGCGCTAACC 1360 SATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGGC 1142 5 TGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC 293 SGGTGAGTAACGCGTGGGAACGTGCCCTTCTCTACGGAATAGCC 127 174 166 ATGAAGGCCTTAGGGTGTAAAGCTCTTTCAGCTGGGAAGA--- 410 AATACCGTATACGCCCTTTGGGGGAAAGATT-------%; Score 828.6; DB 6; Length 1490; %; Pred. No. 1.1e-258; 0; Mismatches 275; Indels 63; Gaps Length 1490; icus or Vibrio alginolyticus US/10/465,448 06-19 0465448

347 CCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGCACTTTCAGTCGTGAAGGAAG	CACTITCAGICGIGAGGAAGG 406		Ov 1445 ACT 1448
	GAAGAAGCCCGGGTAACTCC 448 		1487 ACCT
GTGCCAGCAGCGGGGTAATACGGAGGGGCTAGCGTTGTTCGGAATTACTGG 	TICGGAATTACTGGGGGTAAA 508 	<u>щи.</u>	RESULT 3 PCT-US03-20082-16 ; Sequence 16, Application PC/TUS0320082
GCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAATCCCAGGGCTCAACCTTGGAACTGC 	HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		GENERAL INFORMATION: APPLICANT DOW AGROSCIENCES LLC TITLE OF INVENTION: Paeticidally Active Proteins and Polynucleotides Obtainabl TITLE OF INVENTION: Paenibacillus Species
CTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGGGGGGGATTCCGAGTGTAGAGGTGA 	SAATTCCGAGTGTAGAGGTGA 628 SAATTTCAGGTGTAGCGGTGA 646		FILE REFRENCE: DAS-101XC2 CURRENT APPLICATION NUMBER: PCT/US03/20082 CURRENT FILING DATE: 2003-06-27 PRIOR APPLICATION NUMBER: US 60/392,633
AATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGCTCGATACT(SCTCACTGGCTCGATACTGAC 688 		PRIOR FILING DATE: 2002-06-2 PRIOR APPLICATION UNDER: US PRIOR FILING DATE: 2003-01-2 NUMBER OF SEQ ID NOS: 49
GCTGAGGTGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCACGCCGTA 	ACCTGGTAGTCCACGCCGTA 748 ACCTGGTAGTCCACGCCGTA 766		SOFTWAKE: Patentin ver SEQ ID NO 16 LENGTH: 1547 TYPE: DNA
AACGATGAATGCCAGACGTCGCAAGCATGCTT-GTCGGTGTCACACCTAACGGATTAAG	IGTCACACCTAACGGATTAAG 807 	·· ·· ·· ·· ·· ·· ·· ·· ·· ·· ·· ·· ··	ONGAINDER AFTITICIAL Sequence FEATURE: OTHER INFORMATION: Nucleic acid sequence of the 16S rDNA of IDAS1529. PCT-US03-20082-16
CATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGC	AAGGAATIGACGGGGCCCGC 867 [Query Match 54.0%; Score 784.6; DB 1; Length 1547; Best Local Similarity 74.4%; Pred. No. 2e-244; Matches 1148; Conservative 1; Mismatches 301; Indels 94; Gaps 9;
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGGGGGCGGAGACCTTACCAACCCTTGA 	CAGAACCITACCAACCCITGA 927 	<u> </u>	OY 1 AGTITGAICCIGGCTCAGAACGAGCGTGGCGGCAGGCITAACACATGCAAGTCGAGCGA 60
CATGGCAGGACCGCTGGAGATTCAGCTTTCTCGTAAGAGACCTGCACAGGTGCTGC	AGACCTGCACACAGGTGCTGC 987 		OY 61 GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGT-GG 100
ATGGCTGTCGTCAGCTCGTGTCGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAAC 	TICCGGCAACGAGCGCAACCC 1047 		OY 101 GAACGTGCCCTTCTCTACGGATAGCCCCGGGAAACTGGGGGTAATACGGTATACGCCT 160
ACGICCCTAGITGCCAGCAATTCA-GITGGGAACTCIAIGGAAACTGCCGATGATAAGIC	GGAAACTGCCGATGATAAGTC 1106 		Qy 161 TT
GGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGGCCTTACGGGTTGGGCTACACAGTG 	ACGGGTTGGGCTACACACGTG 1166 		QY 198 TIGGATTAGGTAGTIGGGGTAATGGCCCACCAAGCCGACGACGATCCATAGCTGTTGA 257
CTACAATGGTGGTGACAGTGGGTTAATCCCCAAAAGCC	AATCCCCAAAAGCC 1204 		QY 258 GAGGATGATCAGCCCACTGGGACTGAGACACGGCCAGACCTCTACGGAGCAGCAGT 317 111
ATCTCAGTTCGGATTGTCCTCTGCAACTCGAGGCATGAAGTTGGAATCGCTAGTAAT 	AGTTGGAATCGCTAGTAATCG 1264 		OY 318 GGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCCGCGTGAGTGA
CGGAACAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACCACACCACCGTCACACACCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACACA	ACACACCGCCGTCACACCA 1324		OY 378 CTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAA
TGGGAGTTGGTTCTACCCGACGACGACGCTAACCTTCGGGGGGCAGGCGCCACGGTA	GGGGGCAGCGGCACGGTA 1384 	·	QY 414 -TGACGGTACCAGCAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGGTAATACGG 472
GGATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCGGTAGGGGAACCTGCGGCTGGATC 	AGGGAACCTGCGGCTGGATC 1444 	· ——	QY 473 AGGGGCTAGGGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGT 532 DD 111111111111111111111111111111111111

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                                                                          CAGAAGAGGAAAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGGGAACA
                                                                                                 CCAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAG
                                                                                                            GCAAGATTAAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT
                                                                                                                                                                                                                                                      GCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCAGTGGGAGTATGTGGTTT
                                                                                                                                                                                                                                                                            AATTCGAAGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGAT
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                                                     CGAGAGAGGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACA
                                                                                                                                           CAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGT--CGG
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GENERAL INFORMATION:
APPLICANT: LYANY ANN D.
LYAMICHEV, VICTOR I.
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OLIVE, DAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCGCATGGTTCAAAAGTGAAAGACGGTCTTGCTGTCACTTATAGATGGATCCGCGCTGC
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DETECTION AND IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                    COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release *1,0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/655,378A
FILING DATE: 05-Sep-2000
CLASSIFICATION: <Unknown>
                                                                                    ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 776.8; DB 5;
Pred. No. 6.8e-242;
0; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTTGTAAAGCTCTTTCAGCTGGGAAGATAA----
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                                                                                                                                            STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
21P: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 160:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 705-841
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                             CITY: SAN FRANCISCO
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Best Local Similarity 74.1%;
Matches 1143; Conservative
  INVENTION:
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Sequence 159, Application US/09655378A GENERAL INFORMATION:
                                    APPLICANT: BROW, MARY ANN D. LYAMICHEV, VICTOR I.
                                                                                                                                                                           COUNTRY: UNITED STATES OF
                                                                                                                                                                                                                                                                                           FILING DATE: 05-Sep-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1513 base pairs
                                                                                                                                                                                                                                                                                                                               NAME: CARROLL, PETER G
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 159
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.0%;
Best Local Similarity 73.8%;
Matches 1114; Conservative
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                                                                                                                                                                CALIFORNIA
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                                                                                                   SECUENCES:
                                                                                                   NUMBER OF
US-09-655-378A-159
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                                    CGAAGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGTTCAG
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Ä TIGGIGGGGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTTGAGAGGATGATCAGC 270 CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATCTTAGA 330 -----GGTCTAGCGGCGGACGGGTGAGTAACGCCTGGG-AA 103 72 TGAAGCTICTAGCTTGCTAGAAGTGGATTAGTGGCGCACGGGTGAGTAAGGTATAGTTAA 131 104 CGTGCCCTTCTCTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTT- 162 -------GGGGGAAAGATTTATCGGAGAAGGATCGGCCCGCGTTGGATTAGGTAG 210 12 AGTTTGATCCTGGCTCAGAGTGAACGCTGCCGGCGTGCCTAATACATGCAAGTCGAACGA 71 132 TCTGCCCTACACAGAGACAACAGTTGGAAACGACTGCTAATACTCTATACTCCTGCTT 191 1 AGTITGATCCTGGCTCAGAACGAACGCTGGCGCCAGGCTTAACACAAGTCGAGCGA Gaps 67; Length 1513; OLIVE, DAVID M. TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF Indels MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Score 740.2; DB 5; Pred. No. 4.9e-230; 0; Mismatches 329; SUITE REGISTRATION NUMBER: 32,837 REFERENCE/DOCKET NUMBER: FORS-01756 APPLICATION NUMBER: US/09/655,378 SEQUENCE DESCRIPTION: SEQ.1D NO: 159: US-09-655-378A-159 STREET: 220 MONTGOMERY STREET, CORRESPONDENCE ADDRESS: ADDRESSEE: MEDLEN & CARROLL 372 (331 ð

Oy 1442 ATCACCTCCT 1451 Db 1504 ATCACCTCCT 1513	RESULT 6 US-10-367-794A-3052 ; Sequence 3052, Application US/10367794A ; GENERAL INFORMATION: ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc. ; TITLE OF INVENTION: Streptococcus pneumoniae complete genome. ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333	CURRENT APPLICATION NOMBER: US/10/36/,/94A CURRENT FILING DATE: 2003-02-19 ; NUMBER OF SEQ ID NOS: 3245 ; SOFTWARE: Proprietary ; SEQ ID NO 3052	ENGTH: 1497 TYPE: DNA CRANISM: Streptococcus pneumoniae complete genome.	N: (1974242)(197573 NFORMATION: Chromosome 94A-3052	Query Match Best Local Similarity 73.9%; Pred. No. 2.1e-221; Matches 1090; Conservative 0; Mismatches 295; Indels 90; Gaps 11;	Oy 1 AGTITGAICCTGGCTCAGAACGCTGGCGGGAGGCTTAACACAIGCAAGTCGAGGA 60	Oy 61GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGT-GGGAACG 105	OY 106 TGCCCTTCTCTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGG 165	Oy 166 GGAAAGATTATCGGAGAAGGATCGGCCCGCGTTGGATT 204	OY 205 AGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTTGAGAGGATG 264	OY 265 ATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGCAGGGAAT 324	OY 325 CTTAGACAATGGGGCAACCCTGATCTAGCCGTGAGTGATGAAGGCCTTAGGG 384	OY 385 TIGTAAAGCTCTTCAGCTGGGAAGATAA	OY 419 GTACCAGAGAAGAAGCCCGGGTAACTCCGTGCCAGCAGCGGGGGAAATACGGAGGGGG 478	OY 479 CTAGGGTTGTTGGGATTACTGGGCGTAAAGCGCACGTAGGGAACTGGAAAGTCAGGG 538	OY 539 TGAAATCCCAGGGCTCAACCTTGGAACTTGAAACTATCAGTCTGGAGTTCGAGA 598
391 AGCTCTTTCAGCTGGGAAG-ATAATGACGGTACCAGCAGAAGAAGCCCCGGCTAACTCCG 449 	450 TGCCAGCAGCCGCGTAATACGGAGGGGCTAGCTTGTTCGGAATTACTGGGCGTAAAG 509 11111111111111111111111111111111111	570 TITGAAACTATCAGTCIGGAGTICGAGAGGGGGGGGGTGGATTCCGAGTGTAGAGGTGAA 629 	630 ATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGCGGCTCACTGGCTCGATACTGACG 689	690 CTGAGGTGCGAAAGCGTGGGGGAAACAGGATTAGATACCCTGGTAGTCCACGCGTAA 749 	750 ACGAIGAATGCCAGACGTCGGCAAGCATG-CTTGTCGGTGTCACACCTAACGGATTAAGC 808 	809 ATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCA 868 	869 CAAGGGGTGGAGCATGGGTTTAATTCGAAGCAAGGGGGAGAACCTTACCAACCTTGAC 928 	929 AIGGCAGGACGCTGGAGAGATTCAGCTTTCTCGTAAGAGACCTGCACAGGTG 983 	984 CTGCATGGCTGTCGTCGTGTGAGATGTTCGGTTAAGTCCGGCAACGAGCGCA 1043 	1044 ACCCACGTCCCTAGTTGCCAGCAATTCAGTTGGGAACTCTATGGAAACTGCCGATGATAA 1103 	1104 GTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGGCTTACGGGTTGGGCTACACAC 1163 	1164 GTGCTACAATGGTGGTGACAGTGGGTT	1203 CCATCTCAGTTCGCATTGTCCTCTGCAACTCGAGGCATGAAGTTGGAATCGCTAGTAAT 1262 	1263 GGCGGAACAG-CAIGCCGGGGTGAATACGTTCCCGGGCCTTGTACACACGCCCGTCACA 1321 	1322 CCAIGGGAGTIGGTICTACCCGACGACGNIGCGCTAACCTICGGGGGGCAGGCGCCCCG 1381	1382 GIAGGATCAGCGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGG 1441

OY 599 AGGTGAGTGGAATTCCGAGTGTAGAGTGGAATTCGTAGATATTCGGAGGAGCACCAGTG 6	5 658 3 741	; LOC ; OTH US-10-3	LOCATION: (1974242)(1975739) OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 0-367-794A-3053
8=8	A 718	Query Mat Best Loce Matches]	uery Match 49.1%; Score 713.6; DB 6; Length 1497; est Local Similarity 73.9%; Pred. No. 2.1e-221; atches 1090; Conservative 0; Mismatches 295; Indels 90; Gaps 11;
719° GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATG 	3 778	oy.	1 AGTITGATCCTGGCTCAGAACGAACGCTGGCGGGGGCTTAACACATGCAAGTCGAGCGA 60
& - B	1 836 3 921	Qy	61GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGT-GGGAACG 105
OY B37 TTAAAACTCAAAGGAATTGACGGGGCCCCGCACAAGGGGTGGAGCATGTGGTTTAATTCG 8	3 896 ·	oy G	106 TGCCCTTCTTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGG 165
QY 897 AAGCAGAGAACCTTACCAACCCTTGACATGGC-AGGACGCTGGAGATTCAGC 9	5 955 1 1041 ·	oy G	166 GGAAAGATITATCGGAGAAGGATCGGCCCGCGTTGGATT 204
0y 956 TITCTCGTAAGAGACCTGCACAGGGGCTGCATGGCTGTCGTCGTCGTCGTGGGG 1	A 1015	QQ Q	205 AGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACGATCCATAGCTGGTTTGAGAGGATG 264 1
OY 1016 TGTTCGGTTAAGTCCGGCAACCGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTG 1	3 1075 . 3 1159	oy o	265 ATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAAT 324 11
QY 1076 GGAACTCTATGGAACTGCCGATGATAAGTCGGAGGAGGTGTGGATGACGTCAAGTCCT 1	r 1135 1219	çy qa	325 CTTAGACAATGGGGGCAACCCTGATCTAGCCATGCGGTGGAGGATGAAGGCCTTAGGG 384
QY 1136 CATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGG	1175 .	cy Dp	385 TTGTAAAGCTCTTTCAGCTGGGAAGATAA
QY 1176 -TGGTGACAGTGGGTTAATCCCCAAAAGCCA-TCTCAGTTGGGATTGTCCTCTGCAACTC 1	2 1233 1 1339	oy Op	419 GTACCAGCAGAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGGTAATACGGAGGGG 478
QY 1234 GAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTTC 1 	1293	% Q	479 CTAGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGGAAGCGGAAAGTCAGAGG 538
Qy 1294 CCGGGCCTTGTACACACCGCCCGTCACACGGGGTTGGTTCTACCCGACGACGATGC 1	2 1353 A 1459	OZ QQ	539 TGAAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAG 598
OY 1354 GCTAACCTTCGGGGGCAGGCGCACGCTAGGAT 1388 		QQ Dp	599 AGGIGAGTIGGAATTCCGAGTGTGAAATTCGTAGATATTCGGAGGAGGACACCAGTG 658
ULT 7 10-367-7948-3053		oy qq	659 GCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGGTGCGGAAAGCGTGGGGAGCAAAAA 718
; Sequence 30.3, Application US/1036//94A; GENERAL INFORMATION: APPLICANT: Feldmann, Richard J.; Global Determinants, Inc. ; TITLE OF INVENTION: Streptococcus pneumoniae complete genome.		Qy Dp	719 GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATG 778
CURRENT APPLICATION NUMBER: US/10/367,794A ; CURRENT FILING DATE: 2003-02-19 ; NUMBER OF SEQ ID NOS: 3245		. Oy	779 CTTGTCGGTGTCACACCTAACGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGA 836
3053 1497 1497 NA		Oy Op	937 ITAAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCG 896 11
<pre>i ORGANISM: Streptococcus pneumoniae complete genome. ; FEATURE:</pre>		Qy	AAGCACGCGCAGAACCTTACCAACCCTTGACATGGC-AGGACGGCTGGAGAGATTCAGC 9

		385 ITGIAAAGCICITICAGCIGGGAAGAIAA \	419 GTACCAGCAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGTAATACGGAGGGG 478	479 CTAGCGTTGTTCGGAATTACTGGCCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGG 538 	539 IGAAAICCCAGGGCICAACCTIGGAACTGCCTITGAAACTAICAGICTGGAGTICGAGAG 598 	599 AGGIGAGIGGAAITCCGAGIGTAGAGGIGGAAATTCGTAGAIATTCGGAGGAACACCAGIG 658 	659 GCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCCGAAAGCGTGGGGACAAACA 718 	719 GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATG 778 	779 CITGTCGGIGICACACTAACGGAITAAGCATTCCGCCTGGGGAGTACGGTCGCAAGA 836 1	837 ITAAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAĞCATĞGGGTTAATTCG 896 	897 AAGCAACGCGCAGAACCTTACCAACCCTTGACATGGC-AGGACCGCTGGAGAGATTCAGC 955	956 TITCICGIAAGACCIGCACACAGGICCIGCAIGGCIGICGICAGCICGICGIGAGA 1015	1016 IGTICGGITAATICCGGCAACGAGCGCAACCCACGTGCTTGCTGCCACCAATTCAGTIG 1075	1076 GGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCT 1135 	1136 CATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGG	1176 -IGGIGACAGIGGGITAATCCCCAAAAGCCA-TCICAGITCGGAITGICCICIGCAACIC 1233
da Qy	6 6 6	QY	. QZ	oy ob	oy B	Oy Dp	QQ Dp	Qy Db	Oy Dp	oy Db	O _Y	QY Db	Q D	S G	Qy	ογ
	######################################	OY 1136 CATGGCCTTACGGGTTGGGCTACACGTGCTACAATGG1135	Oy 1176 -TGGTGACAGTGGGTTAATCCCCAAAAGCCA-TCTCAGTTCGGATTGTCCTCTGCAACTC 1233	QY 1234 GAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTTC 1293	QY 1294 CCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGTTCTACCCGACGACGNTGC 1353	QY 1354 GCTAACCTTCGGGGGCAGGGGCCACGGTAGGAT 1388	RESULT 8 US-10-367-794A-2845	Sequence 2845, Appli GENERAL INFORMATION: APPLICANT: Feldmann TITLE OF INVENTION:	FILE REFERENCE: JIM Zegeer Law Offices - 703-584-833 CURRENT APPLICATION NUMBER: US/10/367,794A CURRENT FILING DATE: 2003-02-19 NUMBER OF SEQ ID NOS: 3245		y OKGANISM: Streptococcus pneumoniae complete genome. FEATURE: COCHION: (1813570)(1815247) COTHEN INFORMATION; Chromosome = 1 Strand = negative ConnectronObjectNumber = 3472	Query Match 49.1%; Score 713.6; DB 6; Length 1678; Best Local Similarity 73.9%; Pred; No. 2.2e-221; Length 1678; Netche 1000.	1 AGTTGATCCTGGCTCAGAACGAACGCTGGCGCAGGCTTAACACAAGTCGAGGCAAGCCTAACACAAGTCGAGGGAACGAAC	204 AGITICATCCTGGCTCAGGACGACGGGCGGGCGTGCCTAAIACAIGCAAGTAGAACGC 25. 61GACCTTCGGGTCTAGCGGCGGGGGGGGGGGAACGGT-GGGAACG 10:	264 TGAAGGAGGAGGAGCTTGCTCTGGATGAGTTGCGAACGGGTGAGGTAACGCGTAGGTAACC 32. 106 TGCCCTTCTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCTTTGGG 16.	DD 324 IGCCTGGTAGCGGGGGATAACTATTGGAAACGATAGCTAATACCGCATAAGAGTAGATGT 383 Qy 166 GGAAAGATTTATCGGAGAAGGATCGGCCCGCGTTGGATT 204

qq	1461 CCGGIGACGGCAAGCTAATCTCTTAAAGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTC 1520	qa	692 GTATCTTACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCC 751
상 임	1234 GAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTTC 1293 	Qy Bp	479 CTAGCGTTGTTCGGAATTACTGGGGGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGG 538
9 Q	1294 CCGGGCCTTGTACACACCGCCGTCACACATGGAGTTGGTTCTACCCGACGACGACGNTGC 1353	δ da	539 TGAAATCCCAGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAG 598
S d	1364 GCTAACCTTCGGGGGGGGCGCGCGGGAGGAT 1388 	da Oy	599 AGGIGAGTGGAATTCCGAGIGTAGAGTGAAATTCGTAGATATCGGAGGAACACCAGTG 658
RESULT US-10-	SULT 9 -10-367-794A-12	Qy Dp	659 GCGAAGGCGGCTCACTGGCTCGATACTGAGGTGGGGAAAGCGTGGGGAGCAAACA 718
000 000 000 000 000 000 000 000 000 00	Sequence 12. Application US/1036//94A SEGNERAL INFORMATION: APPLICANT: Feldmann, Richard J.; Global Determinants, Inc. TITLE OF INFUNION: Streptococcus pneumoniae complete genome.	QQ QD	719 GGATTAGATACCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGCAAGCATG 778
4 O O E V) CURRENT APPLICATION NUMBER: US/10/367,794A CURRENT FILING DATE: 2003-02-19 NUMBER OF SEQ ID NOS: 3245	Qy Db	779 CTTGTCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGA 836 1051 CGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACGCAAGG 1110
S S	O ID NO 12 LENGTH: 1686 TYPE: DNA	Qy	837 TTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCG 896
	VEMANISM: SIZEPLOCOCCUS pneumoniae complete genome. FERTURE: LOCATION: (15146)(16831) LOCATION: CAROMORION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 0.367.7048.1?	22 Db	897 AAGCAACGCGCAGAACCTTACCAACCCTTGACATGGC-AGGACCGCTGGAGAGATTCAGC 955
	ery j st L	Qy	956 TTTCTCGTAAGAGCCGCACACAGGTGCTGCATGGCTGTCGTCGTCGTGTCGTGGAA 1015
\$ B	1 AGTITGATCCTGGCTCAGAACGAACGCTGGGGCAGCCTTAACACATGCAAGTCGAGCGA 6 AGTITGATCCTGGCTCAGAACGAACGCTGGGGGGCAGGCTTAACACATGCAAGTCGAGCGA 6 AGTITGATCCTGGCTCAGAACGTTGAACATGCAAGACAAGA	Oy .	1016 TGTTCGGTTAAGTCCGGCAACGAGCGCACGTCCCTAGTTGCCAGCAATTCAGTTG 1075
8 8 8	SGGAACG	oy da	1076 GGAACTCTATGGAAACTGCCGATGATAAGTCGGAAGGTGTGGATGACGTCAAGTCCT 1135
o. o.	TGCCCTTCTACGGAATAGCCCCGGGAAACTGGGAGTAATACCGTATACGCCCTTTGGG 	QQ	1136 CATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGG1175
0 y	GGAAAGATTATCGGAGAAGGATCGGCCGCGTTGGATT	QQ	1176 -TGGTGACAGTGGGTTAATCCCCAAAAGCCA-TCTCAGTTGGGATTGTCCTCTGCAACTC 1233
9. Q	AGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACGATCCATACTGGTTTGAGAGGATG	yo da	1234 GAGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATACGTTC 1293
\$ g	ATCAGCACACTGGGACTGAGACACGCCAGACTCCTACGGGAGGCAGCAGTGGGAAT	Oy Dp	1294 CCGGGCCTTGTACACCGCCGGTCACACCATGGGAGTTGGTTCTACCGGACGNTGC 1353
oy Op	CTTAGGG TTCGGA	δ da	1354 GCTAACCTTCGGGGGGCAGGCGCCACGGTAGGAT 1388
충 <u>염</u>	385 TIGTAAAGCICTITCAGCIGGAAGATAA	RESULT 10 US-10-367	RESULT 10 US-10-367-794A-2844 ; Sequence 2844, Application US/10367794A
O.		GENE ; APP	GENERAL INFORMATION: APPLICANT: Feldmann, Richard J.; Global Determinants, Inc. YIFLE OF INVENTION: Streptocoogus pneumonlae complete genome

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COTHER INFORMATION: Chromosome = 1

US-10-367-794A-2994
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FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333 CURRENT APPLICATION NUMBER: US/10/367,794A CURRENT FILING DATE: 2009-02-19
NUMBER OF SEQ ID NOS: 3245
SOFTWARE: Proprietary
SEQ ID NO 2844
LENGTH: 1886
TYPE? DATA
ORGANISM: Streptococcus pneumoniae complete genome.
                                                                                                                                                          Score 713.6; DB.6;
Pred. No. 2.2e-221;
0; Mismatches 295;
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1 LOCATION: (1813570)...(1815255):

1 OTHER INFORMATION: Chromosome --

US-10-367-794A-2844
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APPLICANT: Neeser, Jean-Richard
APPLICANT: Neeser, Jean-Richard
APPLICANT: Stingele, Francesca
APPLICANT: Latty, Zoe
TITLE OF INVERTION: Lactic Acid Bacteria Producing Polysaccharide Similar to thos
TITLE OF INVERTION: Lactic Acid Bacteria Producing Genes
TITLE OF INVERTION: Lactic Acid Bacteria Producing Genes
FILE REFERENCE: 88265-10322
CURRENT APPLICATION NUMBER: US/10/461,990
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 09/548,606
PRIOR APPLICATION NUMBER: CT/FP 98 06636
PRIOR APPLICATION NUMBER: CT/FP 98 06636
PRIOR APPLICATION NUMBER: CH 94 203245.2
PRIOR APPLICATION NUMBER: CH 94 203245.2
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ConnectronObjectNumber 1010 1070 950 623 743 471 143 591 203 651 263 711 323 771 383 830 443 890 503 531 83 GAGAAIGIGCCIICGGGAACCGIGAGACAGGTGCTGCTGCATGGTGCCTTCGTGAGACAGGTGCTGTG GAGGGGGCTAGCGTTCTTCGGAATTACTGGGCGTAÀAGCGGACGTAGGCGGACTGGAAAG TCAGAGGTGAAATCCCAGGGCTCAACCTTGGAACTGTTGAAACTATCAGTCTGGAGT TCGAGAGAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAC CTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGTATGCGGGGAAT **ACCAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGA** AAGCATG-CTTGTCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGGAGTACGGTC TCAGCTTTCTCGTAAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCG TGAGATGTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTC **AGTIGGGAACICIAIGGAAACIGCCGAIGAIAAGICGGAGGAAGGIGIGGAIGACGICAA** AATGACGGTACCAGCAGAAGCCCCGGCTAACTCCGTGCCAGCAGCGGGGTAATACG ATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCGCGGGTAATACG GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACGTCGGC Gaps with 23; депоше Length 1102; complete genome with Sequence 3533, Application US/10367793A
GENERAL INFORMATION:
APPLICAMT Reldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete (FILE REPERENCE: Jim Zegeer Law Offlices - 703-684-8333 CURRENT FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 4126
SOFWARE: Proprietary
SEQ ID NO 3533
LENGTH: 1102 Indels positive Query Match
45.6%; Score 662.6; DB 6;
Best Local Similarity 78.1%; Pred. No. 6.2e-205;
Matches 831; Conservative 0; Mismatches 210; ŧ Strand MG1655 ; LOCATION: (4164692)...(4165793); OTHER INFORMATION: Chromosome - US-10-367-793A-3533 col1 K-12 Escherichia TYPE: DNA ORGANISM: 1 FEATURE: LOCATION: OTHER INFO 1071 891 624 684 412 472 84 532 144 204 652 264 712 324 772 384 831 444 504 951 24 g δ ద g ò 셤 g g à g g ά g ద á D. ò 셤 δy à ò å δ à

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მ	*1229 AACTCGAGGGCATGAAGTGGAATCGCTAGTAATCGCGGAACAGCATGCCGGGGGAATA 1288 	oy O	891 AATTCGAAGCAACGCGCAGAACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAAT 950
දු පු	1289 CGTTCCGGGCCTTGTACACACCGCCGTCACACCATGGGAGTTGGTTCTACCGGACGAC 1348	yo da	951 TCAGCTITCTCGTAAGAGACCTGCACACGGGGCTGCATGGCTGTCGTCAGCTCGTGTCG 1010
b oy	1349 GNTGCGCTAACCTTCGGGGGGCAGGCGGCCACGGTAGGATCAGCGACTGGGGTGAAGTCG 1408 1	δ _γ	1011 TGAGAIGTICGGITAAGICCGGCAACGAGGCAACCCAGGTCCCTAGITGCCAGCAAITC 1070
Oy Dp	1409 TAACAAGGTAGCGTAGGGGAACCTGCGGCTCGATCACCTCCTT 1452 	oy Op	1071 AGTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAA 1130
RESUI US-10 ; Seg	RESULT 15 US-10-367-793A-3357 ; Sequence 3337, Application US/10367793A	ò a	1131 GTCCTCATGGGCTTACGGGTTGGGCTACACGTGCTACAATGGTGGTGACAGTG 1186
GE ;	NERAL INFORMATION: PPLICANT: Feldmann, Richard J.; Global Determinants, Inc. ITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome with ILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333	Q	1187
	CURRENT APPLICATION NUMBER: US/10/367,793A CURRENT FILING DATE: 2003-02-19 NUMBER OF SEQ ID NOS: 4126 SOFFWARE: Proprietary	oy Og	1229 AACTCGAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATA 1288
SEC	EQ ID NO 3357 LENGTH: 1108 TYPE: DNA ORGANISM: Escherichia coll. K-12 MG1655 complete genome with	oy Ob	1289 CGTTCCCGGGCCTTGTACACACCGCCGTCACACCATGGGAGTTGGTTCTACCCGACGAC 1348
S-1	FEATURE: LOCATION: (4033574)(4034681) D-367-793A-3357	oy oy	1349 GNTGCGCTAACCTTCGGGGGGGAGCGGCCACGGTAGGATCAGCGACTGGGGTGAAGTCG 1408
Oue Bes Mat	Query Match Best Local Similarity 78.1%; Pred. No. 6.3e-205; Matches 831; Conservative 0; Mismatches 210; Indels 23; Gaps 2;	oy Op	1409 TAACAAGGTAGCCGTAGGGAACCTGCGCTGGATCACCTCCTT 1452
Oy.	412 AATGACGGTACCAGCAGAAGAAGCCCGGGTAACTCCGTGCCAGCAGCGGGGTAATAGG 471	Searc Job t	ch completed: July 28, 2003, 12:55:52 time : 178 secs
Q7 Dp	472 GAGGGGGTAGCGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAG 531 	,	
Oy Op	532 TCAGAGGTGAAATCCCAGGCCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGT 591 		
oy Oy	592 TCGAGAGAGGTGAQTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAC 651 	·	
QQ QD	652 ACCAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGA 711 		
dy dy oy	712 GCAAACAGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGCGCGCGC		

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core eudicots; rosids
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
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0; Mismatches 226;
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/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1:
total DNA inserted into pHOS1
1 327 c 236 g 255 t
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Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
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/mol_type="genomic DNA"
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ilarity 76.7%;
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                                                                                                                                                                                                                                     Length 899;
                                                                                                                                                                                                                                  Score 686.8; DB 29; Length
Pred. No. 2.4e-178;
0; Mismatches 107; Indels
                                                                                                      /db_xref="taxon:4577"
/clone="zMMBTa032112"
/clone_llb="zM_0.6_1.0_KB*
/note="Vector: pCR4-TOPO; Site_1:
293 c 211 g 213 t
                                                                              DNA

    899
    /organism="Zea mays"
    /mol_type="genomic DN/strain="B73"

                              Location/Qualiflers
                                                                                                                                                                                                                                  tch 47.3%; al Similarity 87.6%; 773; Conservative
Seq primer: TF
Class: sheared
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ACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACG--TCGGCAAGCATGCTTGTCG 785
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="Trol00bpH3"
/db_xref="taxon:3712"
/clone="BONKF40"
/clone="BONKF40"
/clone="lb="Bo_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"
a 338 c 248 g 267 t
                                                                                                                                                                                                                                    190 GGCCCGCGTTGGATTAGGTAGTTGGTGGGGTAATGGCCCACCAAGCCGACGATCCATAGC
                                                                                                                                                                                                                                                1052 GGCTCGCGTCTGATTAGCTAGTGGGTGAGGCAATAGCTTACCAAGGCGATGATCAGTAGC
                                                                                                                                                                                                                                                                                                                                           GCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCCTGATCTAGCCATGCCGCGTGAGTG
                                                                                                                                                                                                                                                                                                                                                          AGGCCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGGGGTG
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                                                                                                                                                                               Length 1053;
                                                                                                                                                                                 Score 588 8; DB 29; Length
Pred. No. 12.8e-151;
0; Mismatches 227; Indels
    eared ends.
Location/Qualifiers
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  Class:
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BONKF40TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKF40,
PE447500
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eudicots; rosids
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651
TGGGCGTAAAGCGTCTGTAGGTGGCTTTTTAAGTCCGCGGCTCAAATCCCAGGGCTCAACC
                                                                         GTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGCT
                                                                                                                                                                                              TTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGGGGAGTGGAATTCCGAGT
                                                650 CTGGACAGGCGGTGGAAACTACCAAGCTTGAGTACGGTAGGGCAGAGGGAATTTCCGGT
                                                                                                                            CGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT
                                                                                                                                                                                 CCACGCCGTAAACGATGAATGCCAGACG - - TCGGCAAGCATGCTTGTCGGTGTCACACCT
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Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudlcotyledons; core eudicots;
Sermatophyta; Magnollophyta; eudlcotyledons; core eudicots;
Sermatophyta; Magnollophyta; Eassicaceae; Brassica.

I (bases 1 to 1053)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other_GSSs: BONKF40TF
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Fax: 301-838-0208
Email: cdtown@tigr.org
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BH705272.1 GI:18787746
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Other GSSs: BOMKA47TR
Contact: Chris Town
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                                                                                                                                                      1016 bp DNA 11near GSS 13-DEC-2002
BONDZ28TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDZ28,
genomic survey sequence.
                                                                                                                                                                                                                                       Brassica oleracea
Brassica oleracea
Brassica oleracea
Busaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1016)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                           GGAAACTGCCGATGATAGTCGGAGGAAGGTGTGGATGACGTCAAGTCCTCATGGGCCTT 1145
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            TGGTTTGAGAGGATGATCAGCCACACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG 309
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/clone="BOND228"
/clone=1bb="Bo_1.6_2.KB_tot"
/note="Vector: PHOSI; Site_1: BstXI; 1.6-2 kb sheared
/note="Vector: PHOSI; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into PHOSI using BstXI linkers"
328 c 239 g 256 t
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Pred. No. 7.7e-151;
0; Mismatches 228; Indels 6;
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1. 1016
//organism="Brassica oleracea"
//mol_type="genomic DNA"
/strain="Tol0000H3"
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                                                                                                                                                                                                                                                                                                                                                                                    Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                 haploid
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                                                                                                                                                                                                               BZ426201.1 GI:26667713
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DNA is from a doubled 1
Seq primer: TF
Class: sheared ends.
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76.78;
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Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-3523
Fax: 301-838-0208
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BH705272 1079 bp DNA 11near GSS 20-FEB-2002 BOMKA4TF BO_2_3_KB Brassica oleracea genomic clone BOMKA47, genomic survey sequence.
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eudicots; rosids
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                                                        GAATAAGCATCGGCTAACTCTGTGCCAGCAGCGGGGTAATACAGAGGATGCAAGCGTTA
                                                                                                                                                                                                                                                 GAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCCAGTGGCGAAGGCC
GAAGAAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGGGCTAGCGTTG
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoj
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
seurosids II; Brassicales; Brassicaceae; Brassica.
I (Bases I to 1079)
Town, C.D., Van Aken, S., Utterback, P., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
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Length 1079;
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                                                                                                                                                     Score 582.8; DB 28;
Pred. No. 1.3e-149;
0; Mismatches 242;
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ilarity 75.5%;
Conservative
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Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 1069)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Opther_GSSs: BONKR59TF
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                     890 GGGGTAAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCA-CCGTTGAGTTTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 581.6; DB 29; Length
Pred. No. 2.8e-149;
0; Mismatches 264; ..Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdtown@tigr.org
DNA is from a doubled haploid provided by
Seq primer: TR
Class: sheared ends.
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BA474941.
GSS.
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1. .1069
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Best Local Similarity 74.4%;
Matches 786; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
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Fax: 301-838-0208
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core eudicots, rosids
                                Tracheophyta
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                                                                          ( Chases 1 to 1106)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1106;
                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                  USA
                                              Spermatophyta; Magnollophyta; eudicotyledons; core; eurosids II; Brassicales; Brassicaceae; Brassica
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Pred. No. 6.8e-149;
); Mismatches 258;
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                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="Tol000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                              9712 Medical Center Drive, Rockville,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                              Class: sheared ends.
Location/Qualifiers
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llarity 74.9%;
Conservative
                                                                                                                                                                  Contact: Chris Town
                 Brassica oleracea
                                                                                                                                 Unpublished
                                                                                                                                                    Other_GSSs:
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BONHES4TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONHES4,
genomic survey sequence.
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B2469058.1 GI:26764665
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                             936 GAACACCAGCTGGAAACGGCTGCTAATACCCCGTAGGCTGAGGAGCAAAAGGAGGAATCC
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DEFINITION ACCESSION VERSION KEYWORDS

GGTGAAATCCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAG

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                                                                            Gaps
                                             Length 1084;
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                                             Score 566.6; DB 29;
Pred. No. 3.8e-145;
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                                                                       AGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAA 419
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1084)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                            AGAGGIGAGIGGAATICCGAGIGIAGAGGIGAAAIICGIAGAIAIICGGAGGAACACCAG
                                                                                                                                                              CAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGCCAGACG--TCGGCAAG
                                                                                                                                                                                                                     CATGCTTGTCGGTGTCACACCTAACGGATTAAGCATTCCGCCTGGGGAGTACGGTCGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                              /Bright form: 13712"
/clone="BONDUS4"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                   TGGCGAAGGCGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-3523
Fax: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq prime: TF
Class: sheared ends.
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1. 1084
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="Tol000DH3"
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BZ439740.1 GI:26695676
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1077 bp DNA linear GSS 13-DEC-2002 BONEQ637R BO_1.6_2_KB_tot Brassica oleracea genomic clone BONEQ63, BA450751 BA450751.1 GI:26721334 GSS.
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1 (bases 1 to 1077)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .067 ATTCAGTTGGGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACG 1126
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                                                                                                                        GGCA--AGCATGCTTGTCGGTGTCACACCCTAACGGATTAAGCATTCCGCCTGGGGAGTAC
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                                  AGTICGAGAGAGGIGAGIGGAATICCGAGIGIAGAGGIGAAAITCGIAGAIATICGGAGG
                                                                 381 AGTACGGTAGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAG
                                                                                                      649 AACACCAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGTCCTCATGGGCCTTACGGGTTGGGCTACACACGTGCTACAATGG 1175
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Brassica oleracea
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Fax: 301-838-0208
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core eudicots; rosids
GGTCGCGATCCCGCGAGGGTGAGCTAACTCCAAAAACCCGTCCCTCAGTCGGATTGCAGG 1024
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using BstXi linkers"
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                                                                                                                                                                                                                                                                                                      Embryophyta;
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DNA is from a doubled haploid provided by Tom Osborn.
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Spermatophyta, Magnoliophyta, eudicotyledons, core,
eurosids II, Brassicales, Brassicaceae, Brassica.
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76.7%; Pred. No. 2.8e-144;
.1ve 0; Mismatches 216; Indels
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/note="Vector: pHOSI; Site_1:
total DNA inserted into pHOSI
227 c 314 g 188 t
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/mol_type="genomic DNA"
/strain="T01000DH3"
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Tel: 301-838-3523
Fax: 301-838-0208
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Contact: Chris Town
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Class: sheared ends.
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                                                                                                                                     /db_xxef="taxon:3712"
/clone="BONBQ63"
/clone=lb="BoL1.6_2_XB_tot"
/note="vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
267 c 342 g 205 t
                                                                                                       355 CATGCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGA--TA
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Pred. No. 1.2e-142;
0; Mismatches 255;
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/mol_type="genomic D/strain="T01000DH3"
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llarity 73.6%;
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BH647750 1054 bp DNA linear GSS 19-FEB-2002 BOWND31TR BO_2_3_KB Brassica oleracea genomic clone BOWND31, BH647750
                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1054)
Town.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
 AACTCGAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAG-CATGCCGCGGTGAAT 1287
                                                             ACGTTCCCGGGCCTTGTACACACCGCCGTCACACCATGGGAGTTGGTTCTACCCGACGA 1347
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                                                                             432 AAGCCCCGGCTAACTCCGTGCCAGCAGCGGGGTAATACGGAGGGGGGCTAGCGTTGTTCG
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linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 1054
/organism="Brassica oleracea"
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/clone="BoMN031"
/clone="lb="bo_2" 3 kB"
/clone="lb="bo_2" 3 kB"
/clone="lb="bo_2" sheared into pHoS1 using BstXI ling
genomic DNA inserted into PHOS1 using BstXI ling
T 201 a 334 c 263 g 256 t
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Tel: 301-838-3523
Fax: 301-838-0208
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Pred. No. 1.7e-142;
0; Mismatches 241;
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llarity 74.4%;
Conservative C
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Matches 778; Conserv
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genomic DNA inserted into pHOS1 using BstXI linkers"
a 327 c 250 g 256 t
                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 549.8; DB 28; Length 1031; larity 73.9%; Pred. No. 1.6e-140; Conservative 0; Mismatches 242; Indels 27;
                                                                                                                      haploid provided by Tom Osborn
                                                  USA.
                                                  MD 20850,
                                            9712 Medical Center Drive, Rockville,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid provided
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1. 1031
/organism="Brassica oleraces"
Unpublished
Contact: Chris Town
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Matches 762; Conserv
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                  TGGTAGTCCACGCCGTAAACGATGAATGCCAGACG - TCGGCAAGCATGCTTGTCGGTGT
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970 CCTGCACACAGGTGCTGCATGGCTGTCGTCGTGTGGTGAGATGTTCGGTTAAGTC 1029
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                                                   GAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAATCCCAGGG
                                                                                                                                                          552 CTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGAGGTGGAAT
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
i eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases 1 to 1044)
Town.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                        CCTCATGGGCCTTACGGGTTGGGCTACACGTGCTACAATGGTGACAGTGGG---- 1188
                                                                                                                                                                                                                  -----TTAATCCCCAAAAGCCATCTCAGTTCGGATTGTCCTCTGCAA 1230
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                                                                                                                                                                                                                                       132 GATCCCGCGAGGGTGAGCTAACTCCAAAAACCCGTCCTCAGTTCGGATTGCAGGCTGCAA 73
                                                  TIGGGAACTCTATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGT
                                                                                                            252 TTTGGAACCCTGAACAGACTGCCGGTGATAAGCCGGAGGAGGTGAGGATGACGTCAAGT
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/note="Vector: pH0S1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pH0S1 using BstXI linkers"
327 c 261 g 257 t
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Pred. No. 1e-136;
0; Mismatches 241; Indels 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Brassica oleracea"
/mol_type-"genomic DNA"
/strain-"rol000DH3"
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/clone="BONKC86"
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Best Local Similarity 73.8%;
Matches 758; Conservative
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732 TGGTAGTCCACGCCGTAAACGATGAATGCCAGACG--TCGGCAAGCATGCTTGTCGGTGT 789
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                                                                                                                                             612.TCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCTC 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910 AACCTTACCAACCCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCTCGTAAGAGA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGGGGAAT
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               GAATTACTGGGCGTAAAGCGCACGTAGGCGGACTGGAAAGTCAGAGGTGAAATCCCAGGG
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Brassica oleracea
Brassica oleracea
Burayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bernatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 995)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotqun sequencing of Brassica oleracea
BH700021 GSS 20-FEB-2002
BOWND50TR BO_2_3_KB Brassica oleracea genomic clone BOWND50,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGTCTGATTAGCTAGTTGGTGAGCCAATAGCTTACCAAGGCGATGATCAGTAGCTGGT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               755 ccgagaggargarcagccacacrgggacrgagacacgcccagacrccracggaggcag 696
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers'
1 330 c 226 g 258 t
                                                                                                                                                                                                                                                                                                                                           Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3523
Fax: 301-838-0208
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Pred. No. 1.9e-136;
0; Mismatches 255; Indels
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1. .995
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"/strain="TO1000DH3"
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/clone="BOMND50"
                               Jenomic survey sequence
                                                               BH700021.1 GI:18775982
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Contact: Chris Town
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